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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 27, 2004, 16:43:13 ; Search time 21 Seconds (without alignments) 3105.612 Million cell updates/sec

US-10-063-688-34 3502 1 MRTVVLIMKASVIEMFLVLL......QYVPRIIQNICTBFNSQPRN 678 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		collagen alpha 3(V			e matrix		alpha 1	alpha 1			hypothetical prote	hypothetical prote	~	hypothetical prote	von Willebrand fac	undulin 1 - human	collagen alpha 1(V	cell surface glyco	hypothetical prote	leukocyte surface	⇁	von Willebrand fac		von Willebrand fac	MOJETO.	CTRP -	n alpha		collagen alphá 1 (V
SUMMARIES	ID	A40020	A37797	A37979	A33809	S66522	CGHU3A	S31212	S78476	A54849	A45974	T28797	T46488	I51027	S42373	VWHU	A40970	A32856	RWHU1B	T23760	S00551	RWHU1C	G00039	S34839	PS0323	A88396	T18397	S04111	S23377	CGHU1A
	DB	7	7	7	N	7	7	7	7	7	N	~	N	7	7	Н	N	-	Н	0	7	Н	~	7	~	7	~	7	N	-
	Query Match Length	3124	3137	496	493	200	3176	1857	1888	2944	1747	567	741	929	3051	2813	843	1019	1153	550	1153	1163	427	1025	414	1286	2098	1022	918	1028
	Query Match	15.8	14.4	14.3	4	14.0	ä	9.5	9.5	9.4	9.4	9.0	8.5	8.0			•	•	•	•	6.5		•			•		6.0		5.9
	Score	554	504.5	501.5	490	490	471.5	331	331	329.5	329	314.5	298	280.5	279	266	262.5	252.5	231	229	229	228	226.5	226.5	213.5	213.5	210.5		209	0
	Result No.	7	7	m	4	2	9	7	œ	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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S21369 T16580 S03308	A35854 C35243 S09646 CGHU2A	IS6126 A45226 A55348 I45914	T19549 A33998 I50807	A45638 S44142
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ALIGNMENTS

	RESULT 1
	collagen alpha 1(XII) chain precursor - chicken
	N;Alternate names: Ilbrochimerin C;Species: Gallus gallus (chicken)
	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Sep-2003 C:Brosssion: Bangos, BladsE. BladsE. b. Banga. S2814. S2254, S28811
	R; Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obar
	J. Cell Biol. 115, 209-221, 1991 A.Title: The complete primary structure of twoe XII collagen shows a chimeric molecule w
	nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
	A;Reference number: A40020; MUID:92011862; РМID:1918137 а дегеняјот: A40020
	A; Molecule type: mRNA
	A; Residues: 1-1124 CXAM; A; Cross-references: GR-DDD824: NID-G22281D: DIDN-RAADD701.1: PID-G222811
	A, Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
	R;Gordon, W.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
	7. Fig. 201. Light. 201. [John 201.] A large multidomain molecule with partial homology to type I A:Title: Type XII collagen. A large multidomain molecule with partial homology to type I
	A;Reference number: A34465; MUID:90062079; PMID:2584192
	A; Accession: A34485
	A; MOLECULE LYPE: MIKNA * money and office of the control of the c
	A:Cross-references: EMBL:J06137; NID:q211284; PIDN:AA48635.1; PID:g211285
	A;Accession: B34485
	A; Molecule type: protein
	A;Residues: 2772-2792;12846-2813 «GORZ» R-Gradon, M K : Garacke, D.R : Olsen, B.R.
	A;Title: Type XII collagen: distinct extracellular marrix component discovered by cDNA c
	A. Archesian A. A. A. A. A. A. A. Mullistan and a second
	A; Molecule type: mRNA
	A;Residues: 2960-2976, F', 2978-3074, AG' < GOR3>
	A;Cross-references: EMBL:11/3/3/5; NID:Sq211664; FIDN:AA448/18.1; FID:Sd11650
	Ajnote; uns aequemen man been reviseu in reference Alivot Rikoch, M.: Bernasconi, C.; Chiquet, M.
	Bur. J. Biochem. 207, 847-856, 1992
	A;Title: A major oligometre iltoroblast proteoglycan identified as a novel large form of
	A; Neteriore immoet: 023021; No.D.: 023021; A. Accession: S23814
	A;Molecule type: protein
	A;Regidues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 <
	K;Dulber, b.; Van Gar KeBr, m. J. Biol. Chem. 262, 17724-17727, 1987
	A; Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-
	A;Accession: S2254
_	otein
	A; Realdues: 2831_2832, 'T', 2834, 'K', 2836-2843;3002-3014 < DUB>
-	K)11ueb, d.; 11ueb, b.

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C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: 10.8ep-1999 #sequence_revision 10.8ep-1999 #text_change 15-Sep-2003
C.SAccession: A37797; A44270; A32674
R.Dollana, R.; Bonaldo, P.; Colombatti, A.
J. Cell Biol. 111, 2197-2205, 1990
A;Title: Wultiple forms of chicken alpha3(VI) collagen chain generated by alternative spacession: A37797; MUID:91035630; PMID:1977751
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A,Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A,Cross-references: GB:MA4282
R;Bonaldo, P.; Russo, V.; Bucciotti, P.; Doliana, R.; Colombatti, A.
B;cohemistry 29, 1245-1254, 1990
A;Title: Structural and functional features of the alpha3 chain indicate a bridging rpl.
A;Reference number: A34270; MUID:90212613; PMID:2322559
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A; Residues: 224-2871 <BON>
A; Cross-references: GB:M24282
A; Notes: the authors translated the codon TTC for residue 1916 as Leu and TTC for residue
R; Bonaldo, P.; Colombatti, A.
Biol. Chem. 264, 20235-20239, 1989
A; Title: The carboxyl terminus of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of collagen VI is a unique management of the chicken alpha3 chain of the chicken alpha3 chain of chicken alpha3 chain of chicken alpha3 chain of the chicken alpha3 chain of chicken alpha3 ch
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C; Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extrace.
C; Reywords: alternative splicing; cell binding; coiled coil; connective tissue; extrace.
F; 26-3137/Product: collagence # status predicted cNNC>
                                                                                                                                                                                                                                                                                                                      585 LP---KKSKPNKRKIMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIAT 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524
                                                                                                                                          416 TIMBKTOOVKV------OVECSRGVDVKADVVFLVDGSYSIGIANFVKVRAFLEVLVKS 468
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Fig. 2027/Domain: von Willebrand factor type A repeat homology <WW02>
Fig. 2027/Domain: von Willebrand factor type A repeat homology <WW02>
Fig. 2027/Domain: von Willebrand factor type A repeat homology <WW03>
Fig. 2027/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027-1400/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027-1400/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027-1400/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027-2007/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027-2007/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027/Domain: von Willebrand factor type A repeat homology <WW05>
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Fig. 2027/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027/Domain: von Willebrand factor type A repeat homology <WW05>
Fig. 2027/Domain: von Willebrand factor type A repeat homology <W005>
Fig. 2027/Domain: von Willebrand factor type A repeat homology von Willebrand Willebrand Millebrand Millebrand Millebrand Millebrand Millebrand Mi
                                            ---HKTLQPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQPVTNLTKE
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A; Remidues: 2151-2199;2792-3137 <BO2>
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F;2803-2846/Domain:
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cell adhesion #status predicted
IXP, homologous to NC4 domain of type IX collagen #status predicted
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F;2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F;2946-3048/Domain: collagenous COL1 #status predicted <COL1>
F;3049-3124/Domain: non-collagenous NL #status predicted <NC1>
F;32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate
F;2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline
Biochim. Biophys. Acta 1171, 97-98, 1992
A;Title: The two splice variants of collagen XII share a common 5' end.
A;Reference number: S28811; MUID:93042014; PMID:1420368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          < FN3 K>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:2751-2902/Domain: collagenous COL2 #status predicted <COL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibronectin type III repeat homology <Pre>
if ibronectin type III 
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A; Status: preliminary
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F;1566-1647/Domain:
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F;1756-1838/Domain:
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F;2028-2110/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P;2119-2199/Domain:
P;2207-2294/Domain:
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Cartilage matrix protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Bate: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 28-Jul-2003
C;Accession: A33809; A26364
R;Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argr J. Biol. Chem. 264, 8126-8134, 1989
A;Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the gene for cartilage matrix brotein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein, a modular protein of the ex A;Title: Structure of the green for cartilage matrix protein of the ex A;Title: Structure of the green for cartilage matrix protein for cartilage matrix protein for cartilage matrix protein for cartilage matrix
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A;Status: preliminary
A;Molecule type: DNA
A;Rosiduse: 1-493 «KIS>
A;Cross-references: GB:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X12350; GB:X12351; (RiArgraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1387
A;Title: Structural features of cartilage marrix protein deduced from cDNA.
A;Reference number: A26364; MUID:87092429; PMID:3025875
                                                                                                                                                                                                                                                                                                                                                    : : | : : | : | : | 1.27 DEHVD------YVBSYSVIEKLSRKFQRAFCVVSDLCATGDHDCEQVCISSPGSYT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 CACHEGFTLNSDGKTCNVCSGGGGSSATDLVFLIDGSKSVRPENFELVKKFISQIVDTLD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587 KKS----KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELBVIATHP 643
                                                                      273 EELSTQSLEPVSLGDPNCK---IDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAG 329
                                                                                                                                                                                                                                                                                                                 NRSGAPN----VVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENB--KQYVVBPN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 DLSFLIDGSTSIGKRRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTN 352
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A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Residues: 78-493 <ARG-
A,Cross-references: GB:M14792, NID:g211545, PIDN:AAA48695.1; PID:g211546
A,Cross-references: GB:M14792, NID:g211545, PIDN:AAA48695.1; PID:g211546
C,Superfamily: matrilin; EGF homology; von Willebrand factor type A repeat
F;37-204/Domain: won Willebrand factor type A repeat homology <VWA1>
F;227-260/Domain: EGF homology <EGF>
F;270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                -----ADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTAIBKITQRGGLSNVGRAISFVTKNFFSKANG
                                                                                                                                                                                                                                                                                                                                                                                                                                           445 FANKAVCRTNGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLNS----
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29.6%; Pred. No. 4e-25;
tive 68; Mismatches 177; Indels
         Mismatches
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         90;
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Matches 125, Conservative
         Conservative
         129;
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A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:g
F;2954-3039/Domain: fibronectin type III repeat homology <FN3>
F;3072-3122/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (Agn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human gene encoding cartilage matrix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQPLVK--RVCDTDRLACSK-----TCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLT
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                                                                                                                                                                                                                                                       DLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTN
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                                                                                                                                                                                                                                                                                                                                                                                                                    209 VGDLVASVRTSMTPEQAGAKGLVKDITAQESADLIFLIDGSDNIGSVNPQAIRDFLVNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEQLFXKSKPNK-----RKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEBL
                                                                                                                                                                                             Gaps
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                                                                                                                                                                                             31;
                                                                                                                             Length 3137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 501.5; DB 2; Length 496; Pred. No. 6.8e-26;
                                                                                                                          14.4%; Score 504.5; DB 2; Length 30.7%; Pred. No. 6.8e-25; ive 87; Mismatches 155; Indels
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A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the humar
A;Reference number: A37979; MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQIAT----DGSFAFTALDIRNLAALRELLLPNI 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%;
28.8%;
                                                                                                                                                                                       Matches 121; Conservative
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Residues: 1-496 <JEN>
Cross-references: GB:J05667
Accession: B37979
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collagen alpha 3(VI) chain precursor [validated] - human
N;Contains: collagen alpha 3(VI) chain, splice form A9/N10(-)
C;Species: Homo eaptens (man)
C;Dete: 21-Nov-1993 #sequence revision 12-Nov-1999 #text change 15-Sep-2003
C;Accession: A59140; S13679; $24465; A57083; S28776; S00245; C31952; C29848; S26510; S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: $24465
A;Molecule type: protein
A;Rolecule type: protein
B;Colombat: protein
A;Rolecule type: protein
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R:Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.J.; Glanville, R.; Ma:
EMBO J. 9, 385-393, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Molecule type: mRNA
A.Residues: 1-30,237-313,'CWM',318-322,'AR',326-1815,'PD',1818-1819,'ID',1822-3176 <CH5
A.Cross-references: EMBL:X52022; NID:g3127925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 cha.
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A;Residues: 32-126, AK',129-136,'L',138-236 <ZA2>
A;Gresidues: 32-126,'AK',129-136,'L',138-236 <ZDN:AB24261.1; PID:g260297
A;Cross-references: GB:S49432; NID:g360296; PIDN:AB24261.1; PID:g260297
R;Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, M.P.
R;Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, M.P.
A;Title: Characterization of three constituent chains of collagen type VI by peptide se
A;Reference number: S00126; MUID:8802944; PMID:3665927
                                                                                                                                                                                                                                                    639
                                                                                                                                                                                                                                                                                             367 DNSFTVSSGARPGAQKVGIVPTDGRSQDYINDAARKAKDLGFKMFAVGVGNAVEBELRBI 426
                                                                                                                                                             247 GSYTCACHEGPTLNSDGKTCMVCRGGGSGSATDLVFLIDGSKSVRPBNPBLVKKFINQIV 306
                                                                                                         KEFELSDTDTRIGAVQYTYEQRLEPGFDKYSSKPDILMAIKRVGYWSGGTSTGAAINFAL 582
                                                                                                                                                                                                                                                       583 BQLPKKS---KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEBLBVI
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A;Note: parts of this sequence were determined by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S13679; MUID:90151612; PMID:1689238
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A59140
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                  640 ATHPARDHSFFVDEFDNLHQYVPRIIQNICTE 671
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submitted to GenBank, May 1998
A;Reference number: A59140
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A; Residues: 2038-2373 < CH4>
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A;Molecule type: DNA
A;Residues: 310-328 <ZAN>
A;Accession: S28776
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A; Residues: 1-3176 <CHU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: matrilin; BGF homology; von Willebrand factor type A repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 RIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNIC 669
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-500 <ASZ>
A,Cross-references: EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163179
C,Genetics:
                                                                                                                                                                                                                                                                                                                GPAGPLMGVVQYGDNPATHFNLXTHTNSRDLKTA1EKTTQRGGLSNVGRAISFVTKNFFS
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                                                                                                                    -----TIEGAAENEKQYVVBPNFANK---AV
                                                                                                                                                                                        159 VQDVSARARQAGIBIFAIGVGRVDMHTLRQIASEPLDDHVDYVESYSVIBKLTHKPQBAP
                                                                                                                                                                                                                                                               --RINGPYSLHVQSWFGLHKTLQPLVKRVCDTDRLACSKTCLN
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F:277-441/Domain: von Willebrand factor type A repeat homology <VWA2>
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F:30-500/Product: cartilage matrix protein #status predicted <MAT>
F:43-210/Domain: von Willebrand factor type A repeat homology <VWAI>
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                                                                                                                    VEEASRLARESGINIFFI-----
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Matches 142; Conservative
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F; 26-3037/Domain: amino-terminal nonhelical #status predicted <AMI).
F; 26-3037/Domain: amino-terminal nonhelical #status predicted <AMI).
F; 26-3037/Domain: von Willebrand factor type A repeat homology <WW01>
F; 240-405/Domain: von Willebrand factor type A repeat homology <WW02>
F; 37-203/Domain: von Willebrand factor type A repeat homology <WW05>
F; 37-802/Domain: von Willebrand factor type A repeat homology <WW05>
F; 37-802/Domain: von Willebrand factor type A repeat homology <WW05>
F; 31-3194/Domain: von Willebrand factor type A repeat homology <WW05>
F; 131-1394/Domain: von Willebrand factor type A repeat homology <WW05>
F; 131-1394/Domain: von Willebrand factor type A repeat homology <WW05>
F; 1434-1599/Domain: von Willebrand factor type A repeat homology <WW05>
F; 1434-1599/Domain: von Willebrand factor type A repeat homology <WW05>
F; 1431-1394/Domain: von Willebrand factor type A repeat homology <WW10>
F; 1431-1394/Domain: von Willebrand factor type A repeat homology <WW10>
F; 1431-1394/Domain: von Willebrand factor type A repeat homology <WW10>
F; 1431-1394/Domain: von Willebrand factor type A repeat homology <WW10>
F; 2038-2373/Region: cell attachment (R-G-D) motif
F; 2148-2156/Region: cell attachment (R-G-D) motif
F; 2370-2372/Region: von Willebrand factor type A repeat homology <WW11>
F; 265-2986/Region: von Willebrand factor type A repeat homology <WW11>
F; 2671-2800/Domain: von Willebrand factor type A repeat homology <WW11>
F; 2671-2800/Domain: von Willebrand 
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',3111-3161/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
',26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
',108,116,202,251,2079,2331,258,2677,2861,3036/Binding site: carbohydrate (Asn) (covale
',2087/Disulfide bonds: interchain #status predicted
',2100,2206,2239,2316,2319/Modified site: 4-hydroxyproline (Pro) #status experimental
',2103,2209,2212,2322,2337/Binding site: carbohydrate (Lys) (covalent) #status experiment
R;Weil, D.; Mattei, M.G.; Passage, E.; Van Cong, N.; Pribula-Conway, D.; Mann, K.; Deutz
Am. J. Hum. Genet. 42, 435-445, 1988
A;Title: Cloning and chromosomal localization of human genes encoding the three chains of
A;Reference number: A29848; MUID:08161046; PMID:3348212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: this sequence cannot be reliably placed and probably represents the results from R; Mayer, U.; Poseckl, E.; Nischt, R.; Specks, U.; Pan, T.C.; Chu, M.L.; Timpl, R. Bur. J. Biochem. 225, 573-580, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 'MRAWIFFLICLAGRALAA',3102-3176 < MAY>
A; Residues: 'MRAWIFFLICLAGRALAA',3102-3176 < MAY
A; Rote: engineered sequence to allow isolation of the Kunitz-type proteinase inhibitor B
R; Arnoux, B.; Merigeau, K.; Saludian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O.;
submitted to the Brookhaven Protein Data Bank, August 1994
A; Reference number: A52812; PDB:1KNT
A; Contents: annotation; K-ray crystallography, 1.6 angstroms, residues 3106-3160
A; Contents: annotation; K-ray crystallography, 1.6 angstroms, residues 3106-3160
C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit sines are 5-hydroxylated and subsequently O-glycosylated.
C; Comment: The fibronectin type III repeat homology domain may be released during proces
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A;Reference number: S48709; MUID:95045506; PMID:7525281
A;Accession: S48709
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A; Cross-references: GDB:119066; OMIM:120250
A; Map position: 2437.3-2437.3
C; Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA), sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
                                                                                                                                                                                                                                     A.Molecule type: mRNA
A.Residues: 2092-2151 «WEI>
A.Residues: 2092-2151 «WEI>
A.Cross-references: GB:M27449; NID:g291919; PIDN:AAAS2057.1; PID:g291920
A.Note: part of this sequence was determined by protein sequencing
R.Jander, R.; Rautenberg, J.; Glanville, R.W.
Fur. J. Biochem. 133, 39-46, 1983
A.Title: Purther characterization of the three polypeptide chains of bovine and human shacession: 826506; MUID:83209648; PMID:6852033
A.Accession: 826510
A.Residues: 'SAIAGVAGVG' «JAN>
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Genetics:
A,Gene: Coll4A1
C,Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
C,Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
C,Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
E,1-28/Domain: signal sequence #status predicted <AMI>F,29-1857/Product: collagen alpha 1(KIV) chain, short form #status predicted <AMI>F,29-10/Domain: sibronectin type III repeat homology <WANI>F,352-433/Domain: fibronectin type III repeat homology <FWNISC>
F,542-525/Domain: fibronectin type III repeat homology <FWNISC>
F,531-707/Domain: fibronectin type III repeat homology <FWNISC>
F,531-707/Domain: fibronectin type III repeat homology <FWNISC>
F,623-707/Domain: fibronectin type III repeat homology <FWNISC>
FWNISC>
F,623-707/FWNISC>
FWNISC>
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A;Residues: 1-1857 <WAE>
A;Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
F;2103,2209,2212,2322,2337/Modified site: 5-hydroxylysine (Lys) #status experimental
F;3111-3161,3120-3144,3136-3157/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467 LHKTLOPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKBPE 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen alpha 1(XIV) chain precursor, short form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C;Accession: S31212
R;Waelchli, C; Trueb, J; Kessler, B.; Winterhalter, K.H.; Trueb, B.
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                                                                                                                                                                                                                                                                                                                                                                                             DLSFLIDGSTSIGKRRPRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 SRDLKTAIEKITQRGGLSNVGRAISFVTKNPPSKANGNRS--GAPNVVVMVDGWPTDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 ERASRLARBSGINIPPITIBGAAENE-KQYVVBPNPANKAVCRTNGFYSLH--VQSWFG-
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                                                                                                                                                                                                                                                                                 Gaрв
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24.8%; Pred. No. 1.4e-13;
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A;Reference number: S31211; MUID:93185668; PMID:8444186
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tive 74; Mismatches 216;
                                                                                                                                                               Query Match 13.5%; Score 471.5; DB 2; Best Local Similarity 30.9%; Pred. No. 1.1e-22; Matches 122; Conservative 86; Mismatches 148;
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24;

276

330

859

us-10-063-688-34.rpr

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: (9.4 Nov-1994 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2003
C;Accession: A54849; PH0644; S16316; I56328; 184686
C;Accession: A54849; PH0644; S16316; I56328; Jütto, J.
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
Biol. Chem. 269, 20255-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alpha1(VI:A;Reference number: A54849; MUID:94127588; PMID:8051117
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A;Residues: 'EFR', 340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1022 TTLPPPTIPPAKEVCKAAK------ADLVFLVDGSWSIGDDNFNKIISFLYSTVGA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        758 LRVVWDISDHNAQOPRVTYLTAKGDRAERAIMVPGRQNTLLLQP------LLPDTBYK 809
                                                                                                                                                                                                                                                                                                                                                                        713 IVGTTAIPTT------VTTTTTTTTTTPKPTIAVRT------GVRNLVIDDETTSS 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 LMG--VVQYGDN---PATHFNLKTHTNSRDLKTAIBKITQRGCLSNVGRAISFVTKNPPS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 TOSL-----EPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIGKQLLADVAQALDIGPAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 KANG----NRSGAPNVVVWWVDGWPTDKVEEASRLAR----ESGINIFFITIEGAAENBKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 VVEPNFANKAVCRTNGFYSL--HVQSWFGLHKTLQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KKSKPNKRKLMILITDGRSYDDVRIPAMAHLKGVITYAIGVAWAAQEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LWSTATYTSSONR-----PRADPGIQRODPSGAAFOKPVGADVSLGLVPKEELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810 VTITPIYADGEGVSVSAPGKTLPLS-----APRNLRVSDEWYNRLRISWD-APPSP
                                                                                                                                                                                                                                                                                                             174 IPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMD-----
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                                                                                                                                                                         9.5%; Score 331; DB 2; Length 1888;
24.8%; Pred. No. 1.4e-13;
tive 74; Mismatches 216; Indels 140;
F;741-823/Domain: fibronectin type III repeat homology <FN3F> 8;32-94/Domain: fibronectin type III repeat homology <FN3G> P;922-1009/Domain: fibronectin type III repeat homology <FN3H> P;922-1009/Domain: fibronectin type III repeat homology <FN3H> P;104(0-1205/Domain: von Willebrand factor type A repeat homology
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                                                                                                                                                                                                      Best Local Similarity 24.84
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1022 TTLPPPTIPPAKEVCKAAK------ADLVFLVDGSWSIGDDNFNKIISFLYSTVGA 1071
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                                                                                                                                                                                                                                                      277 TOSL-----EPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIOKOLLADVAQALDIGPAGP 330
                                                                                                                                                                                                                                                                                                                            859
                                                                                                                                                                                                                                                                                                                                                                                                                                                  860 TMGYRIVYKSINVPGPA----LETFVGD-DINTIL-----ILMLFSGTEYSVKVFAS 906
       ---LWSTATYTSSQNR-----PRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELS 276
                                                                                                                                                                                    -----LLPDTRYK 809
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P;19-1888/Product: collagen alpha 1(KIV) chain, long form #status predicted <P;29-110/Domain: fibronectin type III repeat homology <FN3A>
P;156-320/Domain: fibronectin type III repeat homology <FN3A>
P;35-433/Domain: fibronectin type III repeat homology <FN3B>
P;35-443/Domain: fibronectin type III repeat homology <FN3B>
P;534-614/Domain: fibronectin type III repeat homology <FN3B>
P;534-614/Domain: fibronectin type III repeat homology <FN3B>
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A; Residues: 1-1888 < TRU>
A; Residues: 1-1888 < TRU>
A; Cross-references: EMED: X70793; NID: 9288872; PIDN: CAA50064.1; PID: 9288873
R; Waelchli, C.; Trueb, J; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Bur. J. Biochem. 212, 483-490, 1993
A; Title: Complete primary structure of chicken collagen XIV.
A; Reference number: 831211; MUID: 9318568; PMID: 8444186
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                                                                                                                                                                                                                                                                                                                        810 VTITPIYADGEGVSVSAPGKTLPLS-----APRNLRVSDEWYNRLRISWD-APPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 KANG---NRSGAPNVVVVMVDGWPTDKVBEASRLAR---ESGINIPFITIEGAAENEKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKE
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                                                                                                                                                              440 VVEPNFANKAVCRINGFYSL - - HVQSWFGLHKTLQ -
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A;Reference number: S78476
A;Accession: S78476
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-416,1460-1811,1843-1888 <WAE>
C,Genetics:
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A, Residues: 1472-1659 <GORl>
A, Accession: S20833
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R; Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NCI) domain of collagen VII resembles multidomain adhesion prop
A; Reference number: 156328; MUID:93107742; PMID:1469284
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A; Moseidues: EFR' 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A; Cross-references: GB: S51236; NID: 362308; PIDN: AAB34637.1; PID: 9262309
R; Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
B; Biol. Chem. 264, 3822-3826, 1989
A; Itle: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A; Reference number: A30296; MUID: 89139437; PMID: 2537292
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NyNORCE: defects in this gene can result in dominant and recessive dystrophic epidermolys
A;NORCE: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453699; PIDN:BAA02853.1; PID:g453699 A;Experimental source: keratinocyte
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
                                                                                                                                                        RiParente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, B.A.; Mat
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-16935, 1991
A;fitle: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A;Reference number: S16316; MUID:91334380; PMID:1871109
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A; Molecule type: protein
A; Mesidues: 'A', 1240-1246,'G', 1248-1250,'XE', 1253-1255,'Q', 1257,'E'; 2032,'C', 2034-2041,'A; Moste: two reported peptides cannot be reliably located
R; Greenspan, D.S.
R; Greenspan, D.S.
A; Genet. 2, 273-278, 1993
A; Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous A; Reference number: 148103; MUID:93271985; PMID:8499916
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A;Residues: 815-892,'E',894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
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A;Cross-references: GB:L06862; NID:G388713; PIDN:AAA89196.1; PID:G388714
A;Cross-references: GB:L06862; NID:G388713; PIDN:AAA89196.1; PID:G388714
B;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. US.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly A;Title: onmber: A55255; MUID:94224777; PMID:8170945
A;Contents: annocation
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: GDB:COL7A1; EBR1; EBD1; EB
;Cross-references: GDB:128750; OMIM:120120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: I56328
                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S16316
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 15-Sep-2003
C;Accession: A45974; S30085; $\overline{5}$22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region ns.
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>
A;Residues: 286-494, 'Q', 496-834, 'A', B'. Linsenmayer, T.F.; van der Rest, M.; Mayne, R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, Bur, J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A;Reference number: S17035, MUID:92037585; PMID:1935930
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;287-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;2876-2929/Domain: animal Runitz-type proteinase inhibitor predicted
F;287,2188,2188,264,267,2673/Modified site: 4-hydroxyproline (Pro) #status exper P;2655,5231/Modified site: 5-hydroxylysine (Lys) #status experimental
F;265,5231/Modified site: carbohydrate (Lys) @covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 TLQPLVKRVC------DTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQ 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAINPALEQLF--KKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 FVTNLTKEFB--ISDTDTRIGAVQYTYBQRLBFGFDFKYSSKPDILNAIKRVGYWSGGTST
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A;Status: preliminary
A;Holecule type: markary
A;Residuse: 1-1747 «GER»
A;Residuse: 1-1747 «GER»
A;Reperimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
S;Apte, S.S.
Submitted to the EMBL Data Library, March 1992
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A;Accession: S30085
A;Accession: S30085
A;Accession: S30085
A;Accession: S30085
A;Accession: S30085
A;Residues: 1472-1660 A&PT>
A;References: EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175
Bir. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 QBELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTBFNSQP 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 PEELKRVASQPTSDFFFFVNDFSILRTLLPLVSRRVCTTAGGVP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1(XIV) chain precursor, short form 2 - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 329.5; DB 2; 35.7%; Pred. No. 3.4e-13; tive 37; Mismatches 88;
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Gaps

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ORIPKESSGOOLKIEDVVVGNNIDSHVERVNGSGSGOTEGSGSGDKSGTERSFDASGEGA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 AGPLMGVVQYGD--NPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KANGURSGAPNVVVMVDGWPTDKVBEASRLARESGINIPPITIEGAAENEKQYVVEPNF 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEGRRENFILMYLLTDGYSYDLIBSGARVLRE-------VPNS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 TLKDSNPGLVRPGEFLSDRPQHRSRLTANLEAKKHTEDFVKTPEKRGPVKDCI--YDIGI 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIDGSSSVGTGNFRTVLQFVTNLTKEFBISDTDTRIGAVQYTYBQRLBFGFDKYSSKPDI 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 IPDSSGSL-EKNPOKOLAFAKOLVEOMPISDNATRVGIVOFAGKTKVRVLANFSONKSOL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNAIKRVGYWSGGTSTGAAINPALEQLPKKSK-PNKRKLMILITDGRSYDDVRIPAMAAH 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-567 <GRL:
A;Cross-references: EMBL:UJ9677; PIDN:AAC47957.1; GSPDB:GN00028; CESP:C16E9.1
A;Experimental source: strain Bristol N2; clone C16E9
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C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               172 PPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSP-SAASTTSIPRPQSVGKRSQEMDLWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....DRLACS-----KTCLNSADIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 PPMP--------PTDPPGYDPDSTFDTTPTPAPPSNGLRAPPMPKWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 TATYTSSONRP-----RADPGIORODPSGAAFOKPVGADVSLGLVPKEELSTQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 RPVSLGD-------PNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGP
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R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23035
A;Accession: T46488
                                                                                                                                              C;Genetics:
A;Gene: CRSP:C16B9.1
A;Map position: X
A;Introns: 15/3; 77/3; 132/1; 185/3; 231/1; 271/2; 301/2; 430/3; 509/1
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                                                                                                                                                                                                                                                                                                        9.0%; Score 314.5; DB 2; Length 567; 22.0%; Pred. No. 3e-13; Artive 84; Mismatches 213; Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618 LKGVITYAIGV----AWAAQEBLEVIATHPARDHSFFVDEFDNLHQYVP 662
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A;Experimental source: adult testis; clone DKFZp434J065
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                                                                                                                                                                                                                                                                                                                   Query Match 9.0%
Best Local Similarity 22.0%
Matches 130; Conservative
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A;Residues: 1-741 <AAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 IVGTTAIPTT-----VITTTTTATTPKPIIAVPRT------GVRNLVIDDETTSS 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- LWSTATYTSSQNR-----PRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELS 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMG--VVQYGDN---PATHFNLKTHTNSRDLKTAIBKITQRGGLSNVGRAISFVTKNFFS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWGYRIVYKSINVPGPA----LETFVGD-DINTIL-----ILNLFSGTEYSVKVFAS 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KANG---NRSGAPNVVVMVDGWPTDKVBEASRLAR---ESGINIFFITIEGAAENEKQY 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----APRNIRVSDEWYNRLRISWD-APPSP 743
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28797
R;Geisel, C.
submitted to the EMBL Data Library, November 1995
A;Beference number: Z20525
A;Reference number: Z20525
A;Reference number: Z20525
A;Accession: T28797
   A, Molecule type: protein
A, Rolecule type: protein
A, Residues: 1551-1570,1593-1599;1639-1667 <GOR2>
C, Keywords: alternative splicing; coiled coil, extracellular matrix; glycopr
C, Keywords: alternative splicing; coiled coil, extracellular matrix; glycopr
E, 204-00main: fibronectin type III repeat homology <RN3A>
E, 236-317/Domain: fibronectin type III repeat homology <RN3B>
E, 418 498,Domain: fibronectin type III repeat homology <RN3C>
E, 507-591/Domain: fibronectin type III repeat homology <RN3E>
E, 207-591/Domain: fibronectin type III repeat homology <RN3E>
E, 106-798,Domain: fibronectin type III repeat homology <RN3C>
E, 294-1089/Domain: fibronectin type III repeat homology <RN3C>
E, 294-1089/Domain: non-collagenous NC4 #status predicted <NC4>
E, 1111-1352/Domain: non-collagenous NC2 #status predicted <NC4>
E, 151-1553/Domain: triple helical domain COL1 #status predicted <COL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 IPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 329; DB 2; Length 1747; Best Local Similarity 24.8%; Pred. No. 1.7e-13; Matches 142; Conservative 74; Mismatches 216; Indels 140;
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694 UTITPIYADGEGVSVSAPGKTLPLS-
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592 615

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C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence revision 30-Jun-1993 #text change 22-Jun-1999
C;Date: 04-Dec-1986 #sequence revision 30-Jun-1993 #text change 22-Jun-1999
C;Date: 04-Dec-1986 #sequence revision 30-Jun-1993 #text change 22-Jun-1999
C;Accession: A34480; S0377; A37139; S23676; A25286; A25366; S23618; S23645; A94
R;Mancuso, D.J; Tuley, B.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora
A; Ettle: Structure of the gene for human von Willebrand factor.
A;Reference number: A34480; WUID:90062044; PMID:2584182
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A; Residues: 990-1947 cMAD>
A; Residues: 990-1947 cMAD>
A; Cross-references: GB: M60675; NID: g340357; PIDN: AAA61295.1; PID: g553810
A; Note: the authors translated the codon CGC for residue 156 as Gln
B; Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian, Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
A; Fitle: Molecular cloning of the human gene for von Willebrand factor and identification
A; Reference number: S23676; MUID: 87260814; PMID: 3496594
A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1; C;Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin t F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F;754-793/Domain: fibronectin type II repeat homology <2F1>
F;1201-1244/Domain: EGF homology <EGF>
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A;Residues: 1-177 <802>
A;Cross-references: EMBL:X06828
A;Cross-references: EMBL:X06828
Biochemistry 30, 253-269, 1991
A;Tile: Human von Willebrand factor gene and pseudogene: structural analysis and differ A;Reference number: A37139; MUID:91105089; PMID:1988024
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A; Residues: 2731-2813 <COL>
A; Cross-references: EMBL/M16945
A; Cross-references: EMBL/M16945
A; Bonthron, D.; Orr, B.C.; Mitsock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
Nucleic Acids Res. 14, 7125-7127, 1986
A; Hilte: Mucleotide sequence of pre-pro-von Willebrand factor cDNA.
A; Reference number: A25298; MUID:87016349; FMID:3489923
                                                                                                                                                                                                                                                                                                                                     536 AVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFKK---SKPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 RVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRT-VLQFVTNLTKBFBISDTDTRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 K---RKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVA-WAAQBELEVIATHPARDHS
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A;Residues: 1-2813 <MAN>
A;Residues: 1-2813 <MAN>
A;Cross-references: EMBL:M25864
A;Cross-references: EMBL:M25864
Bur. J. Biochem. 171, 51-57, 1988
A;Title: The human von Willebrand factor gene. Structure of the 5' region.
A;Reference number: S02377; MUID:88111704; PMID:2828057
                                                                                                                                                                                                                                          14; Gaps
                                                                                                                                                                                Length 3051;
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                                                                                                                                                                             Query Match

8.0%; Score 279; DB 2;
Best Local Similarity 37.4%; Pred. No. 8.8e-10;
Matches 74; Conservative 37; Mismatches 73.
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A; Residues: 1-470,'V',472-2813 <BON>
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Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII collag
A;Reference number: 151027; MUID:95246925; PMID:7729585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARD 646
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VGWREKARKIAILITDGKSQDDIVAPSKRYADEGIELYAVGIKNADENELKEIASDPDEL 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 15-Sep-2003
C;Accession: 151027
                                                                                                                                                                                                                                             hypothetical protein T20G5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
                                                                                           -----DIGFVIDGSSSVG
                                                                                                                                           KDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVPVIDGSKSLG
                                                                                                                                                                                                     508 TGNFRTVLQFVTNLTKEFEISDTDFRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGY
                                                                                                                                                                                                                                                                                                                      568 WSGGTSTGAAINFALEQLFKK---SKPNKRKL---MILITDGRSYDDVRIPAMAAHLKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-929 <WEI>
A;Cross-references: EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g632648
F;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                    Gaps
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                                 34;
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   29.8%; Pred. No. 5.7e-12; rative 38; Mismatches 88; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fishith, A. Bubilton Data Library, March 1994 submitted to the EMBL Data Library, March 1994 A; Reference number: S42368 A; Accession: S42373 A; Molecule type: DNA A; Residues: 1-3051 <SMI> A; Residues: 1-3051 <SMI> CCOSE-references: EMBL: Z30423; NID: g458479; PID: g458485 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 280.5; DB 2;
31.0%; Pred. No. 1.2e-10;
tive 47; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                        476 KRVCDTDRLACSKTCLNSA------
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Matches 63; Conservative
                              68; Conservative
      Best Local Similarity
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                              Matches
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A;Cross-references: GDB:119125; OMIM:193400
A;Map position: 12p13.3-12p13.2
A;Map position: 12p13.1-12p13.2
A;Map position: 12p13.1-12p13.2
A;Map position: 12p13.2-12p13.2
A;Map position: 12p13.2
A;Map position: 12p13.2
A;Map position: 12p13.2
A;Map position: 12p13.2
A;Map position: 12p2 D;Map position: 12p2 D;Map predicted (SIG)
B;Map position: 12p2 D;Map predicted (SIG)
B;Map predicted (MAI)
B;Map position: 12p2 D;Map predicted (MAI)
B;Map position: 12p2 D;Map predicted (MAI)
B;Map position: 12p2 D;Map predicted (MAI)
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P;1947-2295/Domain: type D repeat 4 <D04>
P;2296-2330/Domain: type B repeat 2 <VB1>
P;2316-2395/Domain: type B repeat 3 <VB2>
P;2316-2399/Domain: type B repeat 3 <VB2>
P;2316-2399/Domain: type B repeat 3 <VB3>
P;2407-2599/Domain: von Willebrand factor type C repeat homology <VWC1>
P;2507-2509/Region: cell attachment (R-G-D) motif
P;251-2515-1514,223,2290,2357,2400,2546,2585,2790/Binding site: carbohydrate (Asn. P;1147/Binding site: carbohydrate (Asn. Covalent) #status at/pical
P;1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                               A,Title: Human von Willebrand factor: a multivalent protein composed of identical subun:
A;Reference number: A23464; WUID:86269892; PMID:3015199
A;Accession: A23464
                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 764-773;2803-2813 <CHO>
R;Dent, J.A.; Bstwwitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
A;Title: Identification of a cleavage site directing the immunochemical detection of mo.
A,Reference number: A36013; MUID:90349604; PMID:2385594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Title: Propolypeptide of von Willebrand factor circulates in blood and is identical to A.Reference number: A60913; MUID:86208144; PMID:3486471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1606-1617 - CBEN>
R;Fay, P. J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.
Science 232, 995-998, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1238 QBPGGLVV-PPTDAPVSPTTLYVRDIS----BP-PLHDFYCSRLLDLVPLLDGSSRLSEA 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1292 BFEVLKAFVVODMAELLRISQKWVRVAVVEYHDGSHAYIGLKDRKRPSBLRRIASQVKYAG 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1352 SQVASTSEVLKYTLFQIPSKI--DRPEASRIALLLMAS-----QEPORMSRN----FV 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 ODPSGAARQKRVGADVSLGLVPKBELSTQSLEPVSLGDPNCK--IDLSFLIDGSTSIGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIBKITQRG
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             A; Molecule type: protein
A; Residues: 764-788, 'A', 790-1471,'D',1473-2813 <TIT>
A; Note: 799-Thr was also found
R; Chopek, M.W.; Girma, J.P.; Puikawa, K.; Davie, B.W.; Titani, K.
Biochemistry 25, 3146-3155, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:387-745/Domain: type D repeat 2 <DD2>
F:698-700/Region: cell attachment (R-G-D) motif
F:64-2813/Product: von Willebrand factor #status predicted <MA2>
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F;275-1443/Domain: von Willebrand factor type A repeat homology
F;1496-1654/Domain: von Willebrand factor type A repeat homology
F;1689-1854/Domain: von Willebrand factor type A repeat homology
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:842-1130,1934-2203/Region: duplication
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788-833,2216-2261/Region: duplication
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Residues: 576-590 <PAY>
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A;Molecule type: mRNA
A;Rosidues: 781-788; A;790-1424 <SHE>
A;Molecule type: mRNA
A;Rosidues: 781-788; A; A;790-1424 <SHE>
A;Rosidues: 781-788; A;790-1424 <SHE>
A;Rotes set S2-62n, 857-Asp, and 1381-Thr were also found
R;Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; G
Science 228, 1401-1406, 1985
A;Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones
A;Reference number: A44178; MUID:85244588; PMID:3874428
A;Residues: 2621-2813 <GIN>
A;Residues: 2731-2813 <GIN>
A;Residues: 2731-2813 <GINA coding for human von Willebrand factor using antibody prob
A;Recession: 807363
A;Molecule type: mRNA
A;Residues: 2731-2813 <VES>
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 2731-2813 <VES>
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 2731-2813 <VES>
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 2531-2813 <VES>
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 2531-2813 <VES>
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 2531-2813 <VES>
A;Accession: S07363
A;Molecule type: mRNA
A;Residues: 253678; MUID:85201687; PMID:3873280
A;Reference number: S23678; MUID:85201687; PMID:3873280
A;Accession: S23678; MUID:85201687; PMID:3873280
A;Accession: S23678; MUID:85201687; PMID:3873280
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A; Residues: 'WA', 739,'C',744-769,'H',771-788,'A',790-803,'S',805-873;1289-1471,'D',1473-
A; Note: the authors translated the codon TCG for residue 2168 as Cys
R; Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
Biochemistry 25, 3164-3171, 1986
A; Title: CDNA sequences for human von Willebrand factor reveal five types of repeated do
A; Reference number: A90504; MUID:86269894; PMID:3488076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1021-1030 <-VEZ>
A; Note: 1021-1030 <-VEZ>
A; Note: 1021-1030 <-VEZ>
B; Shelton-Inlose, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
Biochem. Biophys. Res. Commun. 144, 657-665, 1987
A; Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated A; Reference number: $23618; MUID:87213253; PMID:3495266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: protein
Residues: 23-56 <SH3>
Sadler. J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W.
Soc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
Title: Cloning and characterization of two CDNAs coding for human von Willebrand facto
                                                                                                                                                                 encodes a highly repetitive protei
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R;Titani, K.; Kumar, S.; Takio, K.; Bricsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.
Biochemistry 25, 3171-3184, 1986
                                                                                                                                                                                                                                                                                                                                       <VER>
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A;Accession: S23645
                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
Residues: 1-470,'V',472-483,'R',485-1022,'K',1024-1025,'E',1027-1400
Cross-references: EMBL:X04146
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: this sequence has been revised in reference A91056 R;Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H. EMBO J. 5, 3074, 1986 A;Reference number: A91056
                                                                     R, Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H. EMBO J. 5, 1839-1847, 1986
A, Title: Full-length von Willebrand factor (vWF) cDNA enco
A, Reference number: A91044; WUID:87004550; PMID:3019665
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A; Cross-references: EMBL: X04385
R; Verweii. r
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A; Residues: 2731-2813 < LYN>
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Residues: 1-120 <SH2>
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19;

Gapa

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        427 ITIEGAAENBKQYVVBP----------NPANKAVCRTNGFYSLHVQSWFGLHKTLQPL 474

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Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping.
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N-PSDB; AAZ65009.
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Yuan J;
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Watanabe CK; Smith V,

Membrane-bound proteins and related nucleotide sequences.

Claim 12; Fig 113; 822pp; English

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain by exceening. The PRO sequences have homology with proteins including LDL receptors. TIB ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor furnuncadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

Sequence 678 AA;

Gapa ö Query Match
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0 MRTVVI.TMKASVIEWFLVILVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKLIDPEPIV 60 -

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dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
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                                                                                          Human PRO polypeptide sequence #75
                     AAU29098 standard; protein; 678
                                                                                                                                                                                                                                           28-FEB-2001; 2001WO-US006520
                                                                  18-DEC-2001 (first entry)
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                                                                                                                                                                          Homo sapiens
         RESULT 2
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2000WO-US005601. 2000WO-US005841. 2000US-0187202P. 2000US-0186968P.

02-MAR-2000; 03-MAR-2000; 06-MAR-2000;

01-MAR-2000;

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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of and a control sample of normal cells, whereby a higher level of an amamal include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNP) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also protein can be used to determine the presence of tumours and also cusceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
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                                                                                                                                                                                                                                     Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.
    Godowski PJ, Gurney AL;
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100.0%; Pred. No. 8.4e-307;
tive 0; Mismatches 0;
Goddard A, Go
ood WI, Zhang
                                        Wood WI,
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        Chen J, Desnoyers L,
                                        Smith V, Watanabe CK,
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Matches 678; Conserv
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11.-JAN-2000; 2000US-0175481P.

18-FEB-2000; 2000WO-US004341.

18-FEB-2000; 2000WO-US004342.

22-FEB-2000; 2000WO-US005414.

01-MAR-2000; 2000WO-US005601.

03-MAR-2000; 2000WS-0191007P.

10-MAR-2000; 2000WS-0191007P.

25-AFR-2000; 2000WS-01939397P.

22-MAY-2000; 2000WS-US014042.

05-JUN-2000; 2000WS-US014042.
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Local Similarity 100.0%;
Lee 678; Conservative 0:
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I, Gurney AL,
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N-PSDB; AAF92074.
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Grimaldi CJ,
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 MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKPTVPQINCDVKAGKIIDPEFIV
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07-DEC-1999;
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The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping
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me and
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biology, including use as hybridization probes, and in chromosc
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Godowski
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Goddard A,
Wood WI;
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; Pred. No. 8.4e-307;
0; Mismatches 0;
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Watanabe
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541 YEQRLEFGFDKYSSKPDILMAIKRVGYWSGGTSTGAAINPALEQLFKKSKPNKRKLAHLI
                                                                  YEORLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINPALEOLFKKSKPNKRKLMILI
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Godowski P
Paoni NF;
Wood WI;
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Perrara N, Fong S, Gerber H, Gerritsen MB, Goddard A,
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
ROY MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO1277 (UNQ647) protein sequence SEQ ID NO:179
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17 - AUG - 1999;
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06 - JAN - 2000;
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28 - PEB - 2000;
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20 - MAR - AUG 
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WPI; 2001-032160/04

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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO beginneres. AAF446530 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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                                  PRO polynuclectides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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                                                                                                                                       Claim 12; Fig 113; 935pp; English
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Best Local Similarity 100.0
N-PSDB; AAF44155
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WPI; 2002-731348/79.
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                                                                                            22-PBB-2000;
01-MAR-2000;
30-MAR-2000;
                                                                                                                             23-AUG-2000;
24-AUG-2000;
10-NOV-2000;
01-DEC-2000;
                                                           15-SEP-1999;
15-SEP-1999;
22-DEC-1999;
      24-SEP-1998;
24-SEP-1998;
30-SEP-1998;
06-OCT-1998;
08-MAR-1999;
14-MAY-1999;
                                                                                                              22-MAY-2000;
02-JUN-2000;
                                                                                                                                                                             30-MAY-2001;
                                                                               L8-PBB-2000;
                                                                                      18-PEB-2000;
                                                    01-SEP-1999
Human; secreted protein; transmembrane protein; antirheumatic; antiarthritic; osteopathic; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis.
                                                                                      Human secreted/transmembrane protein PRO1277.
                                              ABG95867 standard; protein; 678 AA.
       661 VPRIIQNICTEFNSQPRN 678
VPRIIGNICTEFNSOPRN 678
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98US-00880310P
98US-00880311P
98US-0088034P
98US-0088034P
98US-0088028P
98US-0088053P
98US-0089053P
98US-0089053P
98US-0099054P
98US-0090648P
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98US-0082797P.
98US-0083495P.
98US-0085579P.
98US-0087759P.
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                                                                         (first entry)
                                                                                                                                           US2002119130-A1
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15-MAY-1998;
02-JUN-1998;
04-JUN-1998;
04-JUN-1998;
10-JUN-1998;
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10 - JUN - 1998;
10 - JUN - 1998;
11 - JUN - 1998;
12 - JUN - 1998;
17 - JUN - 1998;
19 - JUN - 1998;
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24-JUN-1998;
25-JUN-1998;
25-JUN-1998;
26-JUN-1998;
02-JUL-1998;
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26-AUG-1998;
26-AUG-1998;
                                                                        10-DEC-2002
                                                                                                                              Homo sapiens
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18-AUG-1998;
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                                                           ABG95867;
661
                                         ABG95867
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98US-0101743P.
98US-0101916P.
98US-0102570P.
98US-0103449P.
                                     99WO-US005028.
99WO-US010733.
99WO-US012252.
                                                                                                                                                   -US008439.
                                                                   99WO-US020111
99WO-US021090
                                                                                       99WO-US021194
99WO-US030720
                                                                                                                                US004414
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2000W0-L
2000W0-L
2000W0-L
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2000MO-1
2000MO-1
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(GETH) GENENTECH INC.

Godowski PJ; Goddard A, Wood WI; Gerritsen MB, Watanabe CK, Baton DL, Filvaroff E, Grimaldi JC, Gurney AL,

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 34; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
C polypeptide having 80 % sequence identity to a sequence appearing as
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG958513-ABG95914 or their associated signal peptide.
CC extracellular domain of the proteins with their associated signal peptide.
CC cids annowing the proteins with their associated signal peptide.
CC or lacking its associated signal peptide. Also included are the nucleic
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC subpected of containing an A, B, C or D polypeptide. By containing the formation of a A/B, B/P, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide, C is a
CC indicative of the presence of an A, B, C or D polypeptide, C is a
CC indicative of the presence of an A, B, C or D polypeptide, H is a
CC oplypeptide, D is a PRO19760 polypeptide. The sample,
CC where A is a PRO10272 polypeptide, G is a PRO2010 polypeptide, H is a
CC polypeptide, D is a PRO19760 polypeptide. The sample comprises
CC acell suspected of expressing the A, B, C or D polypeptide.
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC to a cell expressing a polypeptide designated as A, B, C or D or B, F, G,
CH Or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC to a cell expressing a polypeptide designated as A, B, C or D or
CC or I, or antibodies against them are useful for modulating a biological
CC corivity of a cell expressing a polypeptide designated as B, B, C or D or
CC B, F, G, H, or I. The cell is killed The proteins are useful for
CC corivity of a cell expressing a polypeptide designated as B, B, C or D or
CC B, F, G, H, or I. The cell is killed and the proteins are useful for
CC designated

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11-DEC-1997;
12-DEC-1997;
17-DEC-1997;
                                  15-APR-2003
                                                                                                                    Homo sapiens
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24-0CT-1997;
24-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
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08-APR-1998;
08-APR-1998;
09-APR-1998;
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17-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-1997
               ABU58474;
    useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence represents a novel secreted or transmembrane protein of the
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                                                                                                                                                                                                                                  MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIV
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                                                                                                                                                                              100.0%; Score 3502; DB 5; Length 678; 100.0%; Pred. No. 8.4e-307; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                        Best Local Similarity 100.
Matches 678; Conservative
                                                                                                                                                           Sequence 678 AA;
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ABU58474 standard; protein; 678 AA.

RESULT 6 ABU58474 ID ABU5

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Human, PRO; cytostatic; tumour, cancer; breast; lung; stomach; liver;
dog; cat; cow; horse; sheep; pig; goat; rabbit; ADBPT;
antibody-dependent enzyme mediated prodrug therapy.
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tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.
                                                                                                 Human secreted/transmembrane protein (PRO) #75.
 ABU84337 standard; protein; 678 AA
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970S-0053266P.
970S-0063426P.
970S-0063121P.
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                                                                02-AUG-2003 (first entry)
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01-APR-1998;
08-APR-1998;
08-APR-1998;
09-APR-1998;
15-APR-1998;
21-APR-1998;
21-APR-1998;
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18 - SBP - 1997;

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29-APR-1998;
05-MAY-1998;
06-MAY-1998;
07-MAY-1998;
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                                                                           GINIFPITIEGAARNEKQYVVEPNPANKAVCRTNGFYSLHVQSWFGLHKTLQPLVKRVCD
                                                                                                                                                                                             TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSPPVDEFDNLHQY
                                          PRADPGIQRODPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
                                                                                                                               BKITQRGGLSNVGRAISFVTKNFPSKAMGNRSGAPNVVVWVDGWPTDKVEBASRLARES
                                                                                                                                               EXITORGGI.SUVGRAI SFVTXNFFSKANGNRSGAPUVVVWWYDGWPTDKVEBASRLARES
                                                                                                                                                                                                                                                   TDRLACSKTCINSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKBFBISDTDTRIGAVQYT
                                                                                                                                                                                                                                                                                      YEQRLEFGPDKYSSKPDILMAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILI
                                                                                                                                                                                                                                                                                                     YEQRLEFGFDKYSSKPDILMAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILI
                                                                                                                                                                                                                                                                                                                                          TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEKLKVIATHPARDHSFFVDEFDNIHOY
 PVTLMQLLAVIVAVATPITLPRPSPSAASTISIPRPQSVGHRSQEMDLWSTATYTSSQNR
                           PRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
                                                                                                                                                                                                                                    TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKRFEISDTDTRIGAVQYT
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97US-0059266P.
97US-0063426P.
97US-0063121P.
97US-0063124P.
97US-006354P.
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17-0CT-1997;
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28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
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100.0%; Pred. No. 8.4e-307;
tive 0; Mismatches 0;
98US - 0096897P

98US - 0095959P

98US - 0097022P

98US - 0097022P

98US - 0097954P

98US - 0097954P

98US - 00979116P

98US - 0098014P

98US - 00980116P

98US - 00988116P

98US - 0098811P

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98US-0103449P.
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Local Similarity 100.
hes 678; Conservative
17-AUG-1998;

18-AUG-1998;

18-AUG-1998;

26-AUG-1998;

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19997; 19997; 19997; 19997; 19997; 19998; 19998; 19998; 19998;		10000000000000000000000000000000000000
31-0CT- 13-NOV- 21-NOV- 24-NOV- 24-NOV- 24-NOV- 11-DEC- 11-DEC- 11-DEC- 11-DEC- 11-MAR- 11-MAR- 20-MAR- 20-MAR- 21-MAR- 31-MAR- 31-MAR- 31-MAR-	31. WAR. 1998 01. APR 1998 01. APR 1998 08. APR 1998 09. APR 1998 10. APR 1998 22. APR 1998 22. APR 1998 22. APR 1998 23. APR 1998 29. APR 1998 29. APR 1998 06. MAY 1998 07. MAY 1998 07. MAY 1998 07. MAY 1998 15. MAY 1998 22. MAY 1998 28. MAY 1998 28. MAY 1998 28. MAY 1998 28. MAY 1998	0.2 UNIV. 0.3 UNIV. 0.3.

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116-JUN-1998 | 17-JUN-1998 | 17-JUN-1998 | 18-JUN-1998 | 1

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ABR65601 standard; protein; 678 AA.
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100.0%; Pred. No. 8.4e-307
ive 0; Mismatches 0;
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98US-0101743P.
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98US-0102240P.
98US-010231P.
98US-0102331P.
98US-0102570P.
98US-0102570P.
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Best Local Similarity 100.
Watches 678; Conservative
23 - SEP - 1998,
23 - SEP - 1998,
23 - SEP - 1998,
24 - SEP - 1998,
24 - SEP - 1998,
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2 RESULT

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Human, PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury, cancer; tumour; disgnosis; advenal tumour; lung; colon; breast; prostate; kidney; rectum; colon; breast; prostate; kidney; rectum; antiarthritic; vulnerary; gene therapy.
                                Human secreted polypeptide PRO1277, SEQ ID NO:150.
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970S-0062250P.
970S-0063212P.
970S-0063121P.
970S-0063121P.
970S-0063544P.
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(first entry)
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24-0CT-1997;
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28-APR-1998;
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22-APR-1998;
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07-MAY-1998; 07-MAY-1998; 15-MAY-1998; 15-MAY-1998; 15-MAY-1998; 15-MAY-1998; 16-MAY-1998; 18-MAY-1998; 18-MAY-1998; 18-MAY-1998; 18-MAY-1998; 18-MAY-1998; 19-UN-1998; 19-UN-
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04-AUG-1998;
10-AUG-1998;
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VOSLSLPRWRESPIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180 120 120 240 9 9 KCPAGCODPKKHVYGTDVYASYSSVCQAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG PVTLMQLLAVTVAVATPTTLPRPSPSAASTTS1PRPQSVGHRSQRMDLWSTATYTSSQNR Gaps ö Length 678; Indele Score 3502; DB 6; Pred. No. 8.4e-307; Mismatches 0; Query Match 100.0%; Sc Best Local Similarity 100.0%; Pr Matches 678; Conservative 0; 98US-0096012P98US-0096687P98US-0096891P98US-0096949P98US-0096949P98US-0096949P98US-0096949P98US-0096949P98US-0097922P98US-0097922P98US-0097923P98US-0099714P98US-0099734P98US-0099734P98US-0099734P98US-0099734P98US-0099734P98US-0099734P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100684P98US-0100751P98US-0100751P98US-0100751P98US-0101751P98US-0101734P98US-0101734P98US-0101734P98US-0101733P98US-0101733P98US-0101733P98US-0101733P98US-0101733P98US-0101733P98US-0101733P98US-0101733P98US-0101733P98US-0101734P98US-0101734P98US-0101734P98US-0101734P98US-0101747P98US-0101747P-10-AUG-1998 17-AUG-1998 17-AUG-1998 17-AUG-1998 18-AUG-1998 18-AUG-1998 18-AUG-1998 18-AUG-1998 26-AUG-1998 26-AUG-1998 26-AUG-1998 26-AUG-1998 10-SEP-1998 10-SEP-1998 10-SEP-1998 10-SEP-1998 10-SEP-1998 10-SEP-1998 11-SEP-1998 61 19 121 121 181 ð සි පී **6** 8 셤 ò

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20-MAR-1998;
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21-APR-1998;
01-APR-1998;
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07-MAY-1998;
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28-APR-1998;
29-APR-1998;
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29-APR-1998;
05-MAY-1998;
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22-APR-1998;
   PRADPGIORODPSGAAROKPVGADVSLGLVPXEELSTQSLEPVSLGDPNCKIDLSFLIDG 300
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tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.
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97US-0063121P.
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17-0CT-1997;
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100.0%; Pred. No. 8.4e-307;
ive 0; Mismatches 0;
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nes 678; Conservative
 23-3EP-1998,
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Length Indels

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24-AUG-1998;
26-AUG-1998;
26-AUG-1998;
   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
                                           ABU58012 standard; protein; 678 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                97135-0049787P

97135-0062210P

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98US-0089598P.
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                                                                                                               14-APR-2003 (first entry)
                                                                                                                                                    Human PRO polypeptide #44
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17-OCT-1997;

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16-JUN-1998;
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  GINI FFITI BGAARNEKQYVVEPNFANKAVCRTNGFYSLLHVQSWFGLHKTLQPLVKRVCD
                                                    PRADPGIQRQDPSGAAPQKPVGADVSLGLVPKEELSTQSLBPVSLGDPNCKIDLSFLIDG
                                                                                                     STSIGKRRFRIQKQLLADVAQALDIGPAGFLMGVVQYGDNPATHFNLKTHTNSRDLKTAI
                                                                                                                               STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI
                                                                                                                                                                     EKI TORGGISINGRA I SFVTKNIPSKANGNIR SGAPNVVVVMVDGWPTDKVERASRLARES
                                                                                                                                                                                                         GINI PPITIEGAAENEKOYVVEPNPANKAVCRTNGPYSLHVQSWFGLHKTLQPLVKRVCD
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17-OCT-1997;
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25-PRB-1998;
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100.0%; Pred. No. 8.4e-307;
iive 0; Mismatches 0;
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98WG-US025108

99WG-US000106

99WG-US005028

99WG-014304P

99WG-0144758P

99WG-0144758P

99WG-0146222P

99WG-0146222P

99WG-0146222P

99WG-0146322P

99WG-0146328P

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2000WO-US004414.
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2000WO-US005841.
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2000MO-US007377
2000MO-US013358.
2000MO-US013705.
2000MO-US014941.
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2000MO-US0164941.
2000MO-US015264.
2000MO-US015264.
2000MO-US020317P.
98US-0097955P.
98US-0097974P.
98US-0097974P.
98US-0097978P.
98US-0098014P.
98US-0098014P.
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15 - MAY - 2000;
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22 - MAY - 2000;
23 - MAY - 2000;
24 - MAY - 2000;
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26 - JUL - 2000;
27 - JUL - 2000;
28 - JUL - 2000;
21 - AUG - 2000;
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15-SEP-1999;
16-SEP-1999;
08-OCT-1999;
30-NOV-1999;
01-DEC-1999;
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16-DEC-1999;
05-JAN-2000;
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11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
26-AUG-1998;
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26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
31-AUG-1998;
16-SEP-1998;
16-SEP-1998;
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9805-008885BP.
9805-0088861P.
9805-0089105P.
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98US-0088810P.
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15-MAR-2000;
20-MAR-2000;
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22-MAY-2000;
30-MAY-2000;
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20 - MAR - 1998;

28 - MAY - 1998;

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2000WO-US023522.
2000WO-US02328.
2000WO-US032678.
2000WO-US06520.
2001WO-US016620.
2001WO-US019692.
2001WO-US01780.
2001WO-US01735.
      2000WO-US022031
  28-JJL-2000;
11-AUG-2000;
23-AUG-2000;
24-AUG-2000;
08-NOV-2000;
01-DEC-2000;
28-FEB-2001;
                           01-JUN-2001;
                              20-JUN-2001;
                                  29-JUN-2001;
                                     09-JUL-2001;
28-AUG-2001;
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(GETTH) GENERATECH INC.

Godowski PJ; Paoni NP; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Perrara N, Fong S, Gerber H, Gerritsen NE, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier NA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang

WPI; 2003-247083/24. N-PSDB; ABX80239.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer creatments.

Claim 12; Fig 113; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO CC polypeptides are useful in detecting PRO polypeptides in a sample, in modulating a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO convented by the polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus polypeptide. PRO1312 stimulates processing a PRO536, pro943, PRO926, PRO9137 induce -cfos in endothelial growth, and PRO536, pro943, PRO926, PRO9136 induce -cfos in endothelial cells, and are thus cuseful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating conditions or disorders where angiogenesis would be concerned tumours. PRO912 inhibitis vascular conditions of the propertied are angential for treating conditions of timulated proliferation of endothelial growth factor (VRGF) stimulated proliferation of endothelial growth factor (VRGF) stimulated proliferation of endothelial growth would be beneficial in inhibiting tumour growth. PRO926, CR PRO1068, PRO1184, PRO9136 and PRO1135 endothelial cell growth in response. PRO928, PRO926, PRO9132 is also enhances survival of retinal neurons cells (PRO1132 is also enhances survival) prospected of sorders are useful for treating kidney disease or coher compropathies associated with dermalian kidney mesangial cells, and therefore are useful for treating kidney disease or coher cepaciated with dermalian serial propathies associated with dermalian propagation of cherace of thus useful for treating sporte injuries, and arthritis. This is the construction such a protein and proves in the profession and provession of a novel human PRO protein

Sequence 678 AA;

1 MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV 60 Gape °; 100.0%; Score 3502; DB 6; Length 678; 100.0%; Pred. No. 8.4e-307; 0; Indels 0; Mismatches Best Local Similarity 100. Matches 678; Conservative Local Similarity Query Match ð

61 KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120

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970S-0065311P

970S-0066770P

940S-0066770P

940S-008312P

940S-0084600P

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PRADPGIQRQDPSGAARQKPVGADVSLGLVPKRELSTQSLEPVSLGDPNCKIDLSFLIDG
                                                                                                                                                                                                                                                                                                                                                                           STSIGKRRFRIGKQLLADVAQALDIGPAGPLAGVVQYGDNPATHFNLKTHTNSRDLKTAI
                                                                                                                                                                                                                                                                              PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNR
                                                                                                              PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNR
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97US-0062250P.
97WO-US020069.
97US-0065186P.
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17-OCT-1997;
05-NOV-1997;
12-NOV-1997;
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Q9cy21 mus musculu
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Q8cy16 homo sapien
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sp_bacteria:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
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sp_phage:*
sp_phage:*
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sp_rvirus:*
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sp_vertebrate:*
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Maximum DB seq length: 200000000
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Perfect score:
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Q8n2m7 homo sapien O88493 mus musculu Q8nde6 homo sapien Q96ft5 homo sapien Q80x19 mus musculu	Q99k64 mus musculu Q8r542 mus musculu Q8ce01 mus musculu O97566 canis famil Q7yrk8 canis famil Q63870 mus musculu Q43853 homo sanien	caenc caenc caenc mytil mytil homo bomo	homo homo homo homo homo o gall caenc caenc caenc caenc
Q8N2M7 Q88493 Q8NDE6 Q96FT5 Q80X19	Q99K64 Q8R542 Q8CE01 Q97566 Q7YRK8 Q63870	041853 081562 081562 081605 000261 096AA0	Q8WXVB Q9HQV3 Q9HQV3 Q8CF44 Q8CFZ8 Q9CZA0 Q9CA0 Q9C4N4 Q21281 Q97925
41441	11119911	4 N N N N 4 4 4	.44441120000
488 2657 1016 937 1797	956 956 721 1253 2944	517 644 673 733 733 755 755	954 957 1626 2813 1472 2104 2104 419
11.7 10.8 10.3 10.2	<u> </u>	, o, o o o o o o o	000000000000000000000000000000000000000
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ALIGNMENTS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhin1; Hominidae; Homo.
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Submitted (DBC-1999) to the EMBL/GenBank/DDBJ databases.
REMBL, ACO07363; AAF19243.1;
REMBL, ACO07363; AAF19243.1;
InterPro; IPR004043; LCCL_dom.
RINterPro; IPR004043; LCCL_dom.
RINterPro; IPR002035; VWF_Ā.
R PÉam; PP000925; VWF,Ā.
R PÉam; PR000925; VWFADOWAIN.
R SWART; SW00603; LCCL; 1.
R SWART; SW00603; LCCL; 1.
R PROSITE; PS50827; VWFA. 2.
R PROSITE; PS50824; LCCL; 1.
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Cordes M., Kalicki J., Ames M.;
"The sequence of Homo sapiens BAC clone RP11-294Lil.";
"The sequence of Homo sapiens BAC clone AP11-294Lil.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to Coch-5B2.
WUGSC:H_NH0294L11.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulston J.E., Waterston R.; "Toward a complete human genome sequence."; Genome Res. 8:1097-1108(1998).
                                                                           678 AA
                                                                                                                                                              Created)
                                                                           PRT;
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MEDLINE=99063792; PubMed=9847074;
                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
                                                                           PRELIMINARY;
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GDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHF 345
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Xamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
A Kimura K., Matsuo K., Nakamura Y., Sakine M., Kikuthi H., Kanda K.,
A Magatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
A Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
YMEDO human cDNA sequencing project.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO56772; BAB71279.1;
CGenew, HGKC12697; VIT.

Remi, PRO3815; LCCL, dom.
InterPro; IPR002035; VWP_A.
Pfam; PP03815; LCCL; 1.
Pfam; PP03815; LCCL; 1.
PRINTS; PR00453; VWPADMAIN.
SNART; SM0063; LCCL; 1.
SNART; SM0027; VWA; 2.
SNART; SM00227; VWA; 2.
SNART; SM0021; VWA; 2.
SNART; SM0051; LCCL; 1.
SNART; SM0051; LCCL; 1.
SNART; SM0051; LCCL; 1.
SNART; SM0051; LCCL; 1.
                                                                                                                                                                                                                                                                                                               PRADPGIQRQDPSGAAFQKPVGADVSL------GLVPKRBLSTQSLRPVSL
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                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                             693;
                                                                                                                                                                                                                           Query Match
99.5%; Score 3484.5; DB 4; Length
Best Local Similarity 97.8%; Pred. No. 2.4e-241;
Matches 678; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                al protein.
693 AA; 75575 MW; 2DE8B2421F2D496D CRC64;
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                                                                                                                     61 KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120
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TISSIE-Placenta;
Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Watanabe M., Pujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                           TDRIACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYT
                                                                             1 MRTVVLIPMKASVIEMPLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV
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                                                                   1 MRTVVLTMKASVIEMPLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV
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                          678;
                         100.0%; Score 3502; DB 4; Length 100.0%; Pred. No. 1.3e-242;
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     9870E75A218C686C CRC64;
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     73930 MW;
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                                   Best Local Similarity 100.
Matches 678; Conservative
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519 YEORLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILI
                                                      TOGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBELEVIATHPARDHSPFVDEFDNLHQY
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Liu J., Ren Z.-X., Takanogu M., Mayne R.;
Submitted (DEC-2001) to the RMBL/GenBank/DDBJ databases.
RMBL, AF454755, AAL57848.1; -.
R InterPro; IPR004043; LCCL dom.
InterPro; IPR004043; LCCL, dom.
R Pfam; PR03815; LCCL; 1.
R Pfam; PR00902; vwa; 2.
R PRINTS; PR00453; vWPADOMAIN.
R SWART; SW00603; LCCL; 1.
R SWART; SW0037; vWA; 2.
R PROSITE; PS50820; LCCL; 1.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 PVTLMQLLAVTVAVATPTTLPRDSPSAASTTSIPRPQSVGHRSQEMDLWSTATTTSSQNR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 PRADPGIQRQDPSGAAFQKPVGADVSLGLVPKBELSTQSLEPVSLGDPNCKIDLSFLIDG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRRVAGQSGYKGSYSNG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 EKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVMVDGWPTDKVBEASRLARES 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 YEQRLEFGPDKYSSKPDILNAIKRVGYWSGGTSTGAAINPALEQLFKKSKPNKRKLMILI 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 STSIGKRRFRIQKQLLADVAQALDIGPAGPLAGVQYGONPATHFNLKTHTNSRDLKTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRITVVLIMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPBFIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels 22; Gaps
                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.5%; Score 3344; DB 4; Length 656; Best Local Similarity 96.0%; Pred. No. 2.7e-231; Matches 651; Conservative 1; Mismatches 4; Indels 22
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

TISSUE=Skeletal muscle, and Fetal heart;

Ren Z.-X., Liu J.G., Mayne R.;

"Human vitrin complete cDNA sequence.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF063833; AAL18263.1;

InterPro; IRR004043; LCCL dom.

InterPro; IRR002035; VWF_A.

Pfam; PF00192; Vwa; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 AA; 71767 MW; B242B00DFB07CF2C CRC64;
                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                               Created)
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0453; VWFADOWAIN.
SMART; SM00603; LCCL; 1.
SMART; SM00327; VWR; 2.
PROSITE; PS50820; LCCL; 1.
PROSITE; PS50234; VWFA; 2.
SEQUENCE 656 AA; 71767 MW;
                                                                                             01-DEC-2001 (TEMBLrel. 19, 01-DEC-2001 (TEMBLrel. 19, 01-MAR-2003 (TEMBLrel. 23, Vitrin,
                                                        PRELIMINARY;
                                                                                                                                                                                                                                                  Homo sapiens (Human).
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541 YEQRLEFGFDKYSSKPDILMAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILI 600
                                                                                                                                                                                                                                                                                                               601 TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQY 660
                                                                                                                                                                                                                                                                                                                             420
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                                                                                                                                                                                                                        515 YEQRLERGEDEYSTXSDVLNAIKRVGYWSGGTSTGAAIHYALEQLPKKSKPNKRKLMILI 574
                       274
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            481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLTKEFBISDTDTRIGAVQYT
PRADPGIQRODPSGAAFOKPVGADVSLGLVPKEELSTQSLBPVSLGDPNCKIDLSFLIDG
                                                   STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI
                                                              361 EKITORGGLSNVGRAISFVTKNPPSKANGNRSGAPNVVVVMVDGWPTDKVBEASRLARES
                                                                                                                                                       421 GINIPPITIEGAAENEKOYVVEPNPANKAVCRTNGFYSLHVOSWFGLHKTLQPLVKRVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-Retina;
Strausberg R.;
Submitted (JUL-2002) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00603; LCCL; 1.
SWART; SM00327; VWA; 2.
PROSITE; PS50820; LCCL; 1.
PROSITE; PS5082034; VWFA; 2.
SEQUENCE 650 AA; 70699 MW; 1641623E11003B4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 2801; DB 11;
80.5%; Pred. No. 2.5e-192;
tive 40; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               650
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                                                                                                                                                                                                                                                                                                                                                                                   635 VPKVIQNICTBFNSQPRN 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, BC034120; AAH34120.1; -. MGD; MGI:1921449; Vit. InterPro; IPR004043; LCCL dom. InterPro; IRR002035; VWF A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Cr
01-OCT-2002 (TrEMBLrel. 22, La
01-JUN-2003 (TrEMBLrel. 24, La
RIKEN CDNA 2810429K11 gene.
VIT OR 2810429K11RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.5% Matches 548; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03815; LCCL; 1.
Pfam; PF00092; vwa; 2.
    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNR 240
  QYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINPALEQLFKKSKPNKRKLM 597
                                                                                                                     598 ILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNL 657
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. (1712—1913; Max. 1913); Max. 1911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
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80.5%; Score 2818; DB 6; Length 652;
Best Local Similarity 79.8%; Pred. No. 1.5e-193;
Matches 541; Conservative 49; Mismatches 62; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVIVITOAPGITALBATHTILPKPSPSAGSTASGLRPQPAGQRSKDL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Retina;

TISSUE=Retina;

Ren Z.-X., Liu J.G., Mayne R.;

Ren Z.-X., Liu J.G., Mayne R.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF063832; AAL18262.2; -.

InterPro; IPR004043; LCCL, dom.

R InterPro; IPR004043; LCCL, 1.

R PRIMTS; PR004052; VWF A.

R PRIMTS; SW00403; VWFADOMAIN.

R SMART; SW00603; LCCL; 1.

SMART; SW00603; LCCL; 1.

R PROSITE; PS50234; VWFADOMAIN.

R PROSITE; PS50234; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70872 MW; 3512421CA6987C51 CRC64;
                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                 658 HOYVPRIIONICTEPNSOPRN 678
                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TEMBLrel. 19, 01-MAR-2002 (TEMBLrel. 20, 01-MAR-2003 (TEMBLrel. 23, Vitrin.
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  taurus (Bovine).
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PROSITE; PS50234; VWFA; 2.
SEQUENCE 650 AA; 70638 MW;
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SEQUENCE FROW N.A.

SEQUENCE FROW N.A.

STRAIN-C57BL/6J; TISSUE-Embryo;

STRAIN-C57BL/6J; TISSUE-Embryo;

STRAIN-C57BL/6J; TISSUE-Embryo;

STRAIN-C57BL/6J; TISSUE-Embryo;

A rakawa T., Bara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Matuda H.A., Ashburner M., Barcalov S., Casawant T.,

Radota K., Matuda H.A., Ashburner M., Barcalov S., Casawant T.,

Ruehl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M.,
                   510 QYTYEQRLEFGFDKYNSKADILSAIRRVGYWSGGTSTGAAIQYALEQLFKKSKPNRRKVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNRPRADPGI QRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLBPVSLGDPNCKI DLSFL
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                                                                                                                                                                                                                                                                                                                                                     IDGSTSIGKRRFRIQKQFLADVVQALDIGPAGPLVGVVQYGDNPATQFNLKTHMVSQDLK
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                                                                              VQSLSLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ
                                                                                                                                                              PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEM---DLWSTATYTSS
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KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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Last sequence update)
Last annotation update)
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VIT OR 2810429KllRIK.
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Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato R., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
Rymathaki Y.;
Rym ō. 120 537 120 329 237 231 297 269 417 389 477 449 509 597 269 657 629 298 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLK 357 9 9 1 MGIVVPTWKASVIEVLLVILVTGIHSNKETPKKTKRPKGTVPQINCDVKAGKIINPEFMV PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEM---DLWSTATYTSS PUTLTQAQATPVAEVTHRSTSK--PPAASVTNSPRPQPVGHRSQEMBEVDGWK-----QNRPRADPGIQRQDPSGAAPQXPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSPL 270 IDGSTSIGKRRFRIQKO*FLA*DVVQALDIGPAGPLVGVVQYGDNPATQFNLKTHMNSQDLK TAIRKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLA RESGINI FFITI EGAAENEKOYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVKR ILITDGRSYDDVRIPAMAAHLKGVITYAIGVAMAAQBELEVIATHPARDHSPPVDEFDNL 1 MRIVVLIMKASVIEMPLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV Gaps 34; 650; Length Indels 03B4823E111A214B CRC64; Query Match 79.8%; Score 2796; DB 11; Best Local Similarity 80.5%; Pred. No. 5.7e-192; Matches 548; Conservative 39; Mismatches 60;

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72 HVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRB 131
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               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-JUN-2003 (TrEMBLrel. 24, Last annotation dattor C homolog (Cochlin, COCH)).
11-JUN-2004 (Sebrafish) (Danio rerio).
11-JUN-2004 (Sebrafish) (Danio rerio).
12-JUN-2004 (Sebrafish) (Danio rerio).
13-JUN-2004 (Sebrafish) (Danio rerio).
14-JUN-2004 (Sebrafish) (Sebrafish) (Danio rerio).
15-JUN-2004 (Sebrafish) (Danio rerio).
16-JUN-2004 (Sebrafish) (Danio rerio).
17-JUN-2004 (Sebrafish) (Danio rerio).
18-JUN-2004 (Sebrafish) (Danio reri
                                                                                                                                     QYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFYXKSKPNKRXLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babbage A.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL586026; CAD58748.1; -.
Interpro; IPR004043; LCCL_dom.
Interpro; IPR002035; VWP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 AA; 60351 MW; 4A3B136747C488P0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          608 YKIAPRIIQNICTBPNSQPRN 628
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PERM: PRO1092; VW2; 2.
PRINTS: PR00453; VWPADOMAIN.
SMART; SM00603; LCCL; 1.
SMART; SM0327; VWA; 2.
PROSITE; PSS020; LCCL; 1.
PROSITE; PSS0234; VWFA; 2.
SEQUENCE 553 AA; 60351 WW;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEM---DLWSTATYTSS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 QNRPRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 -----PG------PVLLD--SGFVPKGELSTQSSEPVPQGDPNCKIDLSFL 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAIEKITQRGGLSNVGRAISFVTKNPPSKANGNRSGAPNVVVVMVDGWPTDKVEBASRLA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESGINIPPITIEGAAENBKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLQPLVKR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 KCPAGCQDPKYHVYGTGVYASYSSVCGAAIHSGVLDNSGGKILVRKVAQQSGYKGSYSNG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CS7BL/6J; TISSUE-Dorsal root ganglion;
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.6%; Score 2682; DB 11; Length 628; 77.7%; Pred. No. 8.2e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50820; LCCL; 1.
PROSITE; PS50234; VWPA; 2.
SEQUENCE 628 AA; 68198 MW; C96C4ACEE9B72480 CRC64;
                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                  628 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Mismatches
                                                                                                                                                                                                           Created)
630 YKIAPRIIQNICTEFNSQPRN 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD, MGJ:1921449; Vit.
InterPro: IRR004043; LCCL dom.
InterPro: IPR002035; VWP_A.
Pfam; PP03815; LCCL; 1.
Pfam; PF00922; Vwa; 2.
PRINTS; PR00653; VWRADOMAIN.
SMART; SM00632; VWA, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK051606; BAC34688.1; -.
                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-JUN-2003 (TrEMBLrel. 24, VITRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 529; Conservative
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    VIT OR 2810429K11RIK.
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SEQUENCE FROM N.A.
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Best Local
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216 BFYLKNFTSAKDVLFALKEVGFRGGNSNTGKALKHTAQKFFTVDAGVRKGIPKVVVVFID 275
                                                                                                                                                                                                     336 WFGTTKYVRPLVQKLCTHEQMMCSKTCYNSVNIAFLIDGSSSVGDSNFRLAKLEFVSNIAK 395
                                                                                                                                                                                                                                                                                                                      396 TPBISDIGAKIAAVQPTYDQRTBFSFTDYSTKENVLAVIRNIRYMSGGTATGDAISPTVR 455
             224 QEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAPQKPVGADVSLGLVPKEELSTQSLEPV 283
                                                                                     -----TPEKK------TPEKK------
                                                                                                                               HFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVVMVD
                                                                                                                                                                                      GWPTDKVERASRLARBSGINIFPITIEGAARNEKOYVVEPNFANKAVCRTNGFYSLHVQS
                                                                                                                                                                                                                                              464 WFGLHKTLQPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTK
                                                                                                                                                                                                                                                                                                       524 BPEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Renopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  617
                                                                                                                                                                                                                                                                                                                                                                                 584 QLFK--KSKPNKRKLMILITDGRSYDDVRIPAMAAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 INCDVKAGKIIDPEFIVKCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKIL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 VRKVAGQSGYKGSYSNGVQSLSLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 VYSLPGRENYSSVDANGIQSQMLSRWSASFTVTKGK------SSTQEATGQA- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- 143
QKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 ETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                      372 VGRAISFVTKNPPSKANGNRSGAPNVVVVVVVVVVVDGWPTDKVEEASRLARESGINIPFITIEG
                                                                                                                                                                                        369 NSVDLGFLIDGSSSVGDGNFRLVLDLLVSIARSFDISDIGSRIGALQFTYDQRMEFNFND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 ITCFTRGLDIRKEKADVLCPGGCPLEEPSVYGNIVYASVSSICGAAVHRGVISNSGGVVR
                432 AAENEKOYVVEPNPANKAVCRINGFYSLHVQSWFGLHKTLQPLVKRVCDTDRLACSKTCL
                                                                                                                               309 PSPERASLVSDQDFMRKAVCKDNEFFFTMPSWFSTNKFVKDLAQKLCSIDQMLCSKTCY
                                                                                                                                                                        NSADIGEVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYBQRLEFGFDK
                                                                                                                                                                                                                                                HVLKDNALRALQKI PYMSGGTATGDAINFAVRSLFKPRSSSNRKFLIIITDGQSYDDVRV
                                                                                                                                                                                                                                                                                          PAMAAHLKGVITYAIGVAWAAQBELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNIC--
                                                                                                                                                                                                                                 552 YSSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.1%; Score 1017.5; DB 4; Length 494; 37.2%; Pred. No. 1.7e-64; ive 90; Mismatches 153; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Coagulation factor C (Limulus polyphemus) homology (Cochlin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007230; AAH07230.1; -.
InterPro; IPR004043; LCCL, dom.
InterPro; IPR002035; VWF A.
Pfam; PP003815; LCCL; 1.
Pfam; PP003815; LCCL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0453; VWPADOMAIN.
SMART; SM00603; LCCL; 1.
SMART; SM00327; VWA; 2.
PROSITE; PSS50234; UCCL; 1.
PROSITE; PSS50234; UCCL; 1.
SRQUENCE 494 AA; 53230 MW; 9920BEF97A0AF2FF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similaricy
nes 214; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 PNCK---IDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATH 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYV 661
'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 PWCRIRPTDILFIIDSSRSVRPSEFQAKVFLSQVIESLDVGANATRVGLVNYASTVKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNLKTHTINSRDLKTAIBKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAP---NVVVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 VDGWPTDKVEBASRLARESGINIFFITIBGAARNE-KQYVVBP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485 ACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
14.6%; Score 512; DB 13; Length 49
Best Local Similarity 29.9%; Pred. No. 3.3e-28;
Matches 129; Conservative 71; Mismatches 174; Indels
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Submitted (FRB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC04714 7, AAN47140.1;
PIN; PT0633, PT0633.
GO; GO:0005509; F:calcium ion binding; IBA.
InterPro; IPR001801; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR0062109; IEGF.
InterPro; IPR0062109; IEGF.
                                                                                                                                                                                           TISSUR=Whole;
Klein S., Strausberg R.;
Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BC054272; BT454272.1; -.
Hypothetical protein.
SEQUENCE 490 Aa; 53728 MW; IDAAC8IECAB91848 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to matrilin 1, cartilage matrix protein 1.
Mus musculus (Mouse).
                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Olfactory epithelium;
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                                         cDNA sequences
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                                                                                                                                                          SEQUENCE FROM N.A.
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                                         and mouse
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AC 080VN
AC 080VN
DT 01-JU
DT 0
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325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 VEPNFANKAVCRINGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLMS- 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......ADIGFVIDGSSSVGTGNFRTVLQFVTNLT 522
                                                                                                                                                                                                                                                                                                                27 SLSLVPOPRGHLCRTRPT------DLVFVVDSSRSVRPVBFBKVKVFLSQVIBSLDV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 SEPODEHVD------YVESYNVIEKLAKKROEAPCVVSDLCATGDHDCEQLCVSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 KBPRISDTDTRIGAVQYTYRQRLEFGFDKYSSKPDILMAIKRVGYWSGGTSTGAAINPAL
                                                                                                                                                                                                                                                                             266 SLGLVPKERLSTQSLRPVSLGDPNCKIDLSFLIDGSTSIGKRRPRIQKQLLADVAQALDI
                                                                                                                                                                                                                                                                                                                                                         326 GPAGPLMGVVQYGDNPATHPNLKTHTNSRDLKTAIBKITQRGGLSNVGRAISFVTKNFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          583 BOLFKKS---KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEBLBVI
                                                                                                                                                                                            14.1%; Score 493; DB 11; Length 500;
28.8%; Pred. No. 7.8e-27;
ive 73; Mismatches 183; Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa; Chordata; (vanio rerio).
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; EC045465; AH445465.1; --
GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IRR001881; EGF_Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR0062105; VWF_A.
                                                                                                                                                         500 AA; 54421 MW; DD034F293479A882 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Similar to cartilage matrix protein (Fragment)
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640 ATHPARDHSFFVDBFDNLHQYVPRIIQNICTE 671
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Pfam; PP00008; BGF; 1.
Pfam; PP000092; vwa; 2.
PRINTS; PR00453; VWFADOMAIN.
SWART; SW00181; BGF; 1.
SWART; SW00179; BGF_CA; 1.
SWART; SW00179; BGF_CA; 1.
PROSITE; PS01186; BGF_2; 1.
PROSITE; PS01186; BGF_2; 1.
PROSITE; PS01186; BGF_2; 1.
                                                                                                                                                                                                                 Best Local Similarity 28.8%
Matches 130; Conservative
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24; Gaps

Length 1182;

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293 DLSPLIDGSTSIGKRRPRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHPNLKTHTN 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 TRIGAVQYTYBQRLRFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINPALBQLF---KK 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| ||:::| : || : : || || || || || || 658 VQIGVVQFSHENKEEPQLATFEMSQSDIAMAIDRMTHIGETTLTGSALTF-VSQYFSPDKG 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 OPLVKRVCDTDRLACSKTCLASADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFBISDTD 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKPNKRKIMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBBLEVIATHPARDHS 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 BASRLARESGINIFFITIEGAAENEKOYVVEPNFANKAVCRTNGPYSLHVQSWFGLHKTL 471
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A Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., A Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., A Yamamoto J., Wakamara Y., Kojima S., Nagahari K., A Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., A Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; NEDO human CDNA sequencing project."; NEDO human CDNA sequencing project."; Submitted (MAR-2002) to the EMEL/GenBank/DDBJ databases.

I. Submitted (MAR-2002) to the EMEL/GenBank/DDBJ databases.

R. InterPro; IPR006209; EGF like.

R. InterPro; IPR006209; WWP.A.

R. Pfam; PP00092; VWP.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 SRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGNR-SGAPNVVVMVDGWPTDKVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 DIYLLIDGSGSTQPTDFHEMKTFLSEVVGMPNÍAPHKVRVGAVQYAĎTWDLEPEISKYSN
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                    13.2%; Score 463; DB 11; Length 1: 32.7%; Pred. No. 4.2e-24; tive 66; Mismatches 167; Indels
                                                                                                                                   PROSITE; PS50234; VWPA; 6.
Hypothetical protein.
SEQUENCE 1182 AA; 130946 MW; CA62P1926A428424 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ90116.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 FFVDEFDNLHQYVPRIIQNICT 670
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                                  PERMI PF00092; vwa; 6.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 6.
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SMART; SMO0181; EGF; 2.
SMART; SMO0327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
      InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.7°
Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 SLGLVPKRBLS------TQSLEPVSLGDPNCK-IDLSFLIDGSTSIGK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 RRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIBKJTQR 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 VGTGNPRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGPDKYSSKPDILNAIKRV 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 GYWSGGTSTGAAINFALEQLF----KKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVI 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 NYMERGTWITGHALSFLVDNSFGPNQGARPGVPKVGIVFTDGRSQDYIGDAAKKAKALGFK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 SIGITPRYSMTLPGFVMILCIMGAQATVDLRQAAMAAGICNTKPTDVVFIVDSSRSVRP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Mature 420:563-573(2002).
EMBL; AKOS4356; BAC35749.1; -.
MGD; MGI:2444259; E330026B02Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HICISTPGSFKCACREGFTLM------NDSRSCS-ACSNAATDVVFLIDGSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 FPI-----TIEGAA---ENBKQYVEPNPANK-----AVC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 GGLSNVGRAISFVTKNPFSKANGNRSG--APNVVVMVDGWPTDKVEBASRLARESGINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----RTNGPYSLHVQSWPGLHKTLQPLVKRVCDTDRLACSKTCLNSA-DIGFVIDGSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                       76; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical von Willebrand factor type A domain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYAIGVAWAAQBELEVIATHPARDHSPPVDBFDNLHQYVPRIIQNICTE
                                                                                                                                                                                                                                 Matrix protein.

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SEQÜENCE 507 AA; 55473 MW; A3E4B46232680B63 CRC64;
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MEDLINE=22354683; PubMed=12466851;
The PANTOM CORSORTIUM,
Pfam; PF00092; vwa; 2.
PRINTS; PROGAS1; WPRDOWNIN.
SMART; SM00181; BGF; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS01186; BGF 2; 1.
PROSITE; PS01186; PGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                              Query Match 13.8%
Best Local Similarity 28.8%
Matches 135; Conservative
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Query Match 12.8%; Score 447.5; DB 4; Length 540;
Best Local Similarity 26.4%; Pred. No. 1.6e-23;
Matches 125; Conservative 77; Mismatches 189; Indels 83; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 KSVRPQNPELVKRPVNQIVDFLDVSPEGTRVGLVQPSSRVRTEPPLGRYGTAAEVKQAVL 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 SCQVRDLCNGVDHGCEFQCVSEGLSYRCLCPEGRQLQADGXSCNRCREGHVDLVLLVDGS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 SSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKFDILNAIK 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          564 RVGYWSGCTSTGAAINFALEQLPKK---SKP---NKRKLMILITDGRSYDDVRIPAMAAH 617
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                                                                                                                                                                                                       333 GVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGNR- 391
                                                                                                                                                                                                                                                                                   392 --SGAPNVVVMVDGWPIDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKA 449
                                                                                                                                                                                                                                                                                                                                                             450 VCRTNGF----YSLHVQS-----WFGLHK---------TLQP--- 473
                                                                                                                                                   618 LKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTE 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : | | : | | | | : | | | | EEGIVMYAVGVGKAVEAELREIASEPAELHVSYAPDFGTWTHILLENIASSICPE 486
Hypothetical protein.
SEQUENCE 540 AA; 59632 MW; 5F9337098E01FBD1 CRC64;
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Search completed: May 27, 2004, 16:47:03 Job time : 54 secs

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JS-09-907-794A-227
APPLICANT
  Sequence 227, App
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3502
1 MRTVVLIMEASVIEMPLVLL.....QYVPRIIQNICTBFNSQPRN 678
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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-125A-227
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US-08-462-128-37
US-08-463-180-37
US-08-001-078A-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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No.
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APPLICANT: Kljavin, Toar J.
APPLICANT: Kljavin, Toar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, Micholas F.
APPLICANT: Pan, Micholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APLICANT: William, ESCOTION TO Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APLICATION NUMBER: US 60/143,048
FRIOR APLICATION NUMBER: US 60/145,698
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-09-08
FRIOR PILING DATE: 1999-09-08
FRIOR APPLICATION NUMBER: PCT/US99/21090
                                                                                                   Appli
                                                                                                                                         Sequence 3, Sequence 4, Sequence 6, Sequen
                                 Sequence
Patent No.
Sequence
                                                              5424399-2

US-08-173-497-3

US-08-286-818-3

US-08-618-3

US-08-618-3

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US-08-618-3

US-08-943-363-3

US-08-943-363-3

US-09-618-3

US-09-618-3

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US-09-618-3

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US-09-13-4

US-08-173-497-4

US-08-173-497-4
-08-476-062A-43
F-US96-01314-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 227, Application US/09907794A
patent No. 663468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Betsein, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Giang
APPLICANT: Gacher, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary E.
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Godowski, Paul J.
Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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92 VYSLPGRENYSSVDANGIQSQMLSRWSASFTVTKGK-----SSTQRATGQA- 137
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276 GWPSDDIBEAGIVAREFGVNVFIVSVAKPIPEELGMVQDVIFVDKAVCRNNGPFSYHMPN 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 32.3%; Score 1129.5; DB 4; Length 550; al Similarity 37.1%; Pred. No. 2.8e-97; 234; Conservative 103; Mismatches 175; Indels 119; Gaps
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PRIOR FULING DAIR: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
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US-09-907-794A-227
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Best Local S
Matches 234
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PRIOR PELICATION NUMBER: PCT/US99/28214
PRIOR PELICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-0
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                              Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                         Tumas, Daniel
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CORGANISM: Homo sapiens
US-09-902-775A-227
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                                                                                                                                       Gaps
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                                                                                             Query Match 32.3%; Score 1129.5; DB 4; Length 550; Best-Local Similarity 37.1%; Pred. No. 2.8e-97; Matches 234; Conservative 103; Mismatches 175; Indels 119;
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; Sequence 227, Application US/09902775A
; Patent No. 6686451
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
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                TYPE: PRT
ORGANISM: Homo sapiens
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                                                      US-09-905-125A-227
LENGTH: 550
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APPLICANT: Yumas, Dannel, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT PILING DATE: 2001-07-10
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
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496 amino acids
             TYPE: amino acid
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                                                                                       | HFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVVMVD 403
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                                                                     284 SIGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPAT 343
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                                                                                                                                                                                                                                                                                     464 WFGLHKTLQPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNPRTVLQFVTNLTK 523
                                                                                                                                                                                                                                                                                                                                                          524 EFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALE 583
                                                                                                                                                                                                                                                                                                                                                                                                                                 584 OLFK--KSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIAT 641
                                   ----PTGKRLKK------TPBKK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Goetinck, Paul F.
APPLICANT: Goetinck, Mehrdad
TITLE OF INVENTION: CARTILAGE MATRIX PROTEIN AND METHODS FOR
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 43
CORRESPONDENCES: Lahive & Cockfield
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
ZIP: 02109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 HPARDHSFFVDEPDNLHQYVPRIIQNICTEF 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIPLCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,096
FILING DATE: 15-7AM-1993
APPLICATION NUMBER: US 07/866,403
PILING DATE: 10-APR-1992
ATOMNE: MAPE: 10-APR-1092
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MGP-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08462128
Patent No. 5686059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELBPAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
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273 KELSTQSLEPVSLGDPNCK---IDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAG 329
                                                                                                                                                                                                                                                                                                                                                                                                                          330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : | : | : | : | : | : | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 NRSGAPN---VVVVMVDGWPTDKVBEASRLARESGINIFFITIBGAABNE--KQYVVBPN 444
                                                                                                                                                                                                                                                                          494 -----ADIGEVIDGSSSVGTGNFRTVLQFVTNLTKBFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 PANKAVCRINGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLNS----
                                                                                                              Gaps
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Length 496;
                                                                                                              Indels
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COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,180
Query Match
14.3%; Score 501.5; DB 1;
Best Local Similarity 28.8%; Pred. No. 2.8e-38;
Matches 129; Conservative 80; Mismatches 178;
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APPLICATION NUMBER: US 08/006,096
FILING DATE: 15-JAN-1993
GLASSIFICATION: 435
PRIOR APPLICATION DATA:
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| Patent No. 5741670
| REMERAL INFORMATION: APPLICANT: Goetinck, Paul F. APPLICANT: TONGRAVI, Mehrdad TITLE OF INVENTION: USB NUMBER OF SEQUENCES: 43
| CORRESPONDENCE ADDRESS: 53 ADDRESSER: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lahive & Coc
STREET: 60 State Street
CITY: Boston
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNPFSKANG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 NRSGAPN---VVVVMVDGWPTDKVBEASRLARESGINIFFITIEGAAENE--KQYVVEPN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFE 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 FANKAVCRTNGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLNS---- 493
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                                                                                                                                                                                                                                                                                         Query Match 14.3%; Score 501.5; DB 1; Length 496; Best Local Similarity 28.8%; Pred. No. 2.8e-38; Matches 129; Conservative 80; Mismatches 178; Indels 61;
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Patent No. 5872094

GREREAL INPORMATION:
APPLICANT: Goetinck, Paul F.
APPLICANT: Tondravi, M., Mehrdad
APPLICANT: Binette, Francois
TITLE OF INVENTION: FORMATION
INTERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      644 ARDHSFFVDRFDNLHQYVPRIIGNICTE 671
                                                   NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-005DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 annino acids
TYPE: amnino acid
TYPE: amnino acid
APPLICATION NUMBER: US 07/866,403
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
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247 CACHEGFTLASDGKTCNVCSGGGGSSATDLVPLIDGSKSVRPENPELVKKFISQIVDTLD 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTALEKITORGGLSNVGRAISFVTKNFFSKANG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527 ISDTDTRIGAVQYTYEQRLÆFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINPALEQLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
14.3%; Score 501.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 2.8e-38;
Matches 129; Conservative 80; Mismatches 178;
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CHEARING SIGILE EXT.
SOFWARE: ASCII LEXT.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,078A
FILING DATE: 06-JAN-1993
CLASSIPICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: MYGES, Paul L.
REGISTRATION NUMBER: 35,965
REFREENCE/DOCKET NUMBER: MGP-008
TELECHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Gorley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Raser, Mathew
ITILE OF INVENTION: HUMAN MATRILIN-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08897443
Patent No. 5981263
                                                                                                                                                                                                                                                                                                                                             LENGTH: 496 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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Sequence 1, Application US/08463218
Patent No. 5986052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 EELSTQSLEPVSLGDPNCK---IDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 NRSGAPN---VVVVMVDGWPTDKVERASRLARESGINIFPITIEGAAENE--KQYVVEPN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 FANKAVCRTNGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLNS---- 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 DEHVD------YVESYSVIEKLSRKFQEAFCVVSDLCATGDHDCEQVCISSPGSYT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527 ISDTDTRIGAVQYTYEORLEFGFDKYSSKPDILMAIKRVGYWSGGFSTGAAINFALBOLF 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587 KKS---KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHP 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        494 ------QPIGFVIDGSSSVGTGNFRTVLQFVTNLTKBFB 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 501.5; DB 2; Length 496; 28.8%; Pred. No. 2.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Mismatches 178; Indels
                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASSES for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 ARDHSFFVDEFDNLHQYVPRIIQNICTE 671
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0348 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-855-0555
         : 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: GenBa
CLONE: 1732121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: link
IMMEDIATE SOURCE
                                                             USA
                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-897-443-4
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RESULT 8 US-08-463-218-1

273 BELSTQSLEPVSLGDPNCK---IDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAG 329 330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNPFSKANG 389 137 : :|:| : |::| 197 DEHVD------YVESYSVIEKLSKKFQRAPCVVSDLCATGDHDCEGVCISSPGSYT 246 247 CACHEGETLASDGKTCAVCSGGGGSSATDLVPLIDGSKSVRPENFELVKKFISQIVDTLD 306 527 ISDIDTRIGAVOYTYEQRLEFGPDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALBQLF 586 390 NRSGAPN---VVVVMVDGWPTDRVBEASRLARESGINIFFITIEGAAENE--KQYVVBPN 444 -----ADIGEVIDGSSSVGTGNFRTVLQFVTNLTXBFB 526 367 TVSSGARPGAQKVGIVPTDGRSQDYINDAAKKAKDLGFKMFAVGVGNAVBDBLRBIASBP 426 445 PANKAVCRINGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLNS---- 493 587 KKS---KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBELEVIATHP 643 77 Gaps Indels 61; Length 496; GENERAL INFORMATION:
APPLICANT: Goetinck, Paul F.
APPLICANT: Tondravi, Mehrdad
APPLICANT: Tondravi, Mehrdad
APPLICANT: Binette, Francois
TITLE OF INVENTION: METHODS FOR PROMOTING CARTILAGE MATRIX
TITLE OF INVENTION: PORMATION
NUMBER OF SEQUENCES:
CORRESPONDENES:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510 Query Match
14.3%; Score 501.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 2.8e-38;
Matches 129; Conservative 80; Mismatches 178; COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,218
FILING DATE: 05-UNRE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,078
FILING DATE: 06-JAN-1993
ATTORNEY/AGENT INFORMATION: NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-008DV
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 1: : 496 amino acids amino acid SEQUENCE CHARACTERISTICS Massachusetts : USA TOPOLOGY: linear MOLECULE TYPE: peptide 494 ઠે

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Desnoyers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 EELSTQSLEPVSLGDPNCK---IDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGCLSNVGRAISFVTKNPFSKANG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : | : | : | : | : | . | : | 197 DEHVD------YVBSYSVIEKGSRKFQEAFCWYSDLCATGDHDCEQVCISSPGSYT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 --------ADIGFVIDGSSSVGTGFRTVLQFVTNLTKRFE 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 FANKAVCRTNGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLNS---- 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 501.5; DB 5; Length 496; 28.8%; Pred. No. 2.8e-38; Live 80; Mismatches 178; Indels 61
                                                                                                                                                                                             TITLE OF INVENTION: METHODS FOR PROMOTING CARTILAGE MATRIX TITLE OF INVENTION: PORMATION
NUMBER OF SEQUENCES: 2
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-JAN-1993
INFORMATION FOR SEQ ID NO: 1:
INFORMATION FOR SEQ ID NO: SEQUENCE LISTING
SEQUENCE CHARACTERISTICS:
                     : | |: : | | : : | | 427 VAEHYPYTADFKTINQIGKKLQKKICVE 454
644 ARDHSPFVDEPDNLHQYVPRIIQNICTE 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 ARDHSPPVDEPDNLHQYVPRIIQNICTE 671
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                                                                                                                                      Sequence 1, Application PC/TUS9400253 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 496 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.89
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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RESULT 10 US-09-907-794A-34 ; Sequence 34, Application US/09907794A

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APPLICANT: Nationary, Mainerary, Mainerary,
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256 APQKPVGADVSLGLVPKBELSTQSLRPVSLGDPNCKIDLSFLIDGSTSIGKRRPRIQKQL 315
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17.9%; Pred. No. 1.9e-25;
Live 81; Mismatches 191; Indels 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PELICATION NUMBER: PCT/USO2
PRIOR PELICATION NUMBER: PCT/USO2
PRIOR PELICATION NUMBER: PCT/USO3
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PLILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-06
PRIOR PELICATION NUMBER: PCT/US99/28564
PRIOR PLILING DATE: 1999-12-06
PRIOR PELICATION NUMBER: PCT/US99/30999
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-07
PRIOR PLILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                      Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.
                                                                                                              Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                                                                                                                                                                                                             Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 17.9*
Matches 139; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-905-125A-34
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                                                                                                                                                                                                                                                                                                                                                                                      560 DGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVPVI 619
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                                                                                                                 256 APOKPVGADVSLGLVPKEELSTQSLRPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQL 315
                                                                                                                                                                                                                                                                                                                                                     376 ISFVTKNPFSKANGN---RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIF----- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 YVCRCKOGYILNSDQFTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDGKRCV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGCEHECVNM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 TCSRVDYCLLSDHGCEYSCVNMDRSPACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSC 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 VSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCRCLEGFRLAE 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KRVCDTDRLACSKTCLNSA------------------DIGFVI 500
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                                                                                                                                                     LADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIBKITQRGGLSNVGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FITIE--GAAENEKQYVVEPNF-----
                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  740 KAKANGITMYAVGVGKAIBEELQBIASEPTNKHLFYAEDFSTWDBISEKLKKGIC 794
Query Match 10.6%; Score 370; DB 4; Length 915; Best Local Similarity 17.9%; Pred. No. 1.9e-25; Matches 139; Conservative 81; Mismatches 191; Indels 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ANKAVCR-----
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APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT PILING DATE: 2001-07-10
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
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| FRIOR APPLICATION NUMBER: PCT/05/97/23099 |
| FRIOR APPLICATION NUMBER: PCT/05/97/28114 |
| FRIOR PILING DATE: 1999-11-29 |
| FRIOR PILING DATE: 1999-11-30 |
| FRIOR FILING DATE: 1999-11-30 |
| FRIOR FILING DATE: 1999-12-02 |
| FRIOR FILING DATE: 1999-12-02 |
| FRIOR FILING DATE: 1999-12-02 |
| FRIOR FILING DATE: 1999-12-06 |
| FRIOR FILING DATE: 1999-12-10 |
| FRIOR FILING DATE: 1999-12-10 |
| FRIOR FILING DATE: 1999-12-10 |
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| FRIOR FILING DATE: 1999-12-30 |
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OR PILING DATE: 1999-11-20
OR PILING DATE: 1999-11-20
OR PILING DATE: 1999-11-30
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OR APPLICATION NUMBER: PCT/US99/28564
OR PILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/US99/28564
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Best Local Similarity 17.94
Matches 139; Conservative
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259
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                                                                                                                                            200 DENTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHPCINIPGS
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qlang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               llan, Kenneth, J
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Mather, Jennie P.
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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Nucleic
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17.9%; Pred. No. 1.9e-25;
ive 81; Mismatches 191; Indels 364; Gaps
Secreted and Transmembrane Polypeptides and Acids Encoding the Same
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us-10-063-688-34.rai

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9.6%; Score 337.5; DB 2;
17.4%; Pred. No. 2.3e-22;
Ive 75; Mismatches 177;
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Parent No. 5848536
GENERAL INFORMATION:
APPLICANT: Garfinkel, Leonard
                                                                                                  17.48;
                                                                                                                     Conservative
          IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 2072792
                                                                                                     Similarity
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US-08-347-594A-2
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Matches 140;
 TOPOLOGY:
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                                                         380 BESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLK 439
                                                                                                                     440 TCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSC 499
                                                                                                                                                                             500 VSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAE 559
                                                                                                                                                                                                             -----DIGFVI 500
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                                                                                                                                                                                                                                                                                                                               561 AIKRVGYWSGGTSTGAAINFALEQLFKK---SKPNKRKL---MILITDGRSYDDVRIPAM 614
                                                                                                                                                                                                                                                                                                                                                           680 AVAHMKYMGKGSMTGLALKHMPERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWAS 739
                                                                                                                                                                                                                                                                                                                                                                                         615 AAHLKGVITYAIGVAWAAQEELBVIATHPARDHSFFVDEFDNLHQYVPRIIQNIC 669
                                                                                                                                                                                                                                                                                                                                                                                                           476 -----KRVCDTDRLACSKTCLNSA-------
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APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Kaser, Mathew
TITLE OF INVENTION: HUMAN MATRILIN-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-897-443-3
; Sequence 3, Application US/08897443
; Patent No. 5981263
; GENERAL INPORMATION:
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REGERENCE/DOCKET NUMBER: PF. TELECOMMUNICATION INPORMATION: TELEPHONE: 415-855-0555
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TYPE: amino acid
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STRANDEDNESS:
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631 CRCSEGPVLAEDGKHCKRCTEGPIDLVPVIDGSKSLGEENFETVKHFVVGIIDSLAVSPK 690
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                                                                                                                                                                                                                                                                                   273 DOKTCRIQDICATEDHGCEQLCVNMLGSFVCQCYSGYTLAEDGKRCTAMDYCASENHGCE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 GCEQLCLANTEESFVCQCSEGFLINDDLKTCSRADYCLLSNHGCEYSCVNTDKSFACQCPE 512
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                                                                                                                                                                           40 MYPOTALLESSCE-----NKRADLVFIIDSSRSVNTYDYAKVKBFILDILQFLDIGPD 92
                                                                                                                                                                                                                                                                                                                                                                                                                 269 LVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPA
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                                                             Gaps
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                                                          Indels 413;
Length 956;
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CLONING AND PRODUCTION OF HUMAN VON
WILLEBRAND FACTOR GPIb BINDING DOMAIN FOLYPEPTIDES AND
METHODS OF USING SAME
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Best Local Similarity 21.9%; Pred. No. 4.6e-15;
Matches 102; Conservative 85; Mismatches 200; Indels 78; Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,594A
FILING DATE: No. 5849536ember 30, 1994
CLASSIFICATION: 435
ATORNEY/ACENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36537-B2
                                                                                                                                                                                                                                                                                                                                   STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                 John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2050 amino acids
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SEQUENCE CHARACTERISTICS
APPLICANT: Richter, Tam.
TITLE OF INVENTION: CLO.
TITLE OF INVENTION: WILL.
TITLE OF INVENTION: METHORSES: 4
CORRESPONDENCE ADDRESS:
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3Y: linear
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368 G-LSNVGRAISFVTKNPFSKANGNRSGAPNVVVVMVDGWPTDKVBBASRLARBSGINIPP 426
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     Sequence 1, Application US/09381261A

Sequence 1, Application US/09381261A

Patent No. 6489290

GENERAL INFORMATION:
APPLICANT: LOSCALO, JOSEPH

TITLE OF INVENTION: No. 6489290el Anti-Platelet Agent
FILE REFERENCE: 10228.327

CURRENT APPLICATION NUMBER: US/09/381,261A

CURRENT PILING DATE: 1999-12-07

FRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1997-03-27

PRIOR PILING DATE: 1997-03-27

WOMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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ALI GNMENTS

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APPLICANT: Zhang, Zemin
TITLE OF INVEXTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
               Sequence 179, Application US/09989722
Patent No. US20020072067A1
                                                                                                                                                                                Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                             Ferrara, Napoleone
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Kljavin, Ivar J.
Napier, Mary A.
                                                 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                     Baker, Kevin P.
Botstein, David
                                                                                                                           Desnoyers, Luc
                                                                                                                                              Eaton, Dan L.
US-09-989-722-179
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FILING DATE: 1997-06-16 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17

NUMBER: 60/065186 1997-11-12 NUMBER: 60/065311 1997-11-24 NUMBER: 60/066770 1998-02-25 NUMBER: 60/075945 11998-02-25 NUMBER: 60/079910 1998-03-20 NUMBER: 60/09910 1998-04-28 NUMBER: 60/094600 1998-04-28 NUMBER: 60/094600	NUMBER: 60/08760 1998-05-28 NUMBER: 60/08760 1998-06-02 1998-06-02 NUMBER: 60/08752 NUMBER: 60/08762 NUMBER: 60/08802 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08802 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04	1998 · NUMBER NUMBER 1998 · NU
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PRIOR FILING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-18
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PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-12
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Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary E.
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Kljavin, Ivar J.
Napier, Mary A.
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Botstein, David
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              PRIOR FILING DATE: 1998-07-01
PRIOR PAPPLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/091544
PRIOR APPLICATION NUMBER: 60/091549
PRIOR PILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091360
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RESULT

Sequence 179, Application US/0969723

FREERIN INFORMATION:

MAPLICANT: Secretion US/0969723

APPLICANT: Secretion US/0969724

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1998-06-23

NUMBER: 60/088033 1998-06-04 NUMBER: 60/088326 1998-06-04 NUMBER: 60/088167 1998-06-05 NUMBER: 60/088202 1998-06-05 NUMBER: 60/088212 1998-06-05 NUMBER: 60/088217 1998-06-05 NUMBER: 60/088217 1998-06-05 NUMBER: 60/088217	~~`~`~`~`~`~`~\~\~\~\~\~\~\~\~\~\~\~\~\	1998-06-17 NUMBER: 60/089801 1998-06-18 NUMBER: 60/089907 1998-06-18 NUMBER: 60/089908 1998-06-18 NUMBER: 60/089948 1998-06-19 1998-06-19 NUMBER: 60/08952 1998-06-19 NUMBER: 60/08952 1998-06-22 NUMBER: 60/090254
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KCPAGCODPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120 181 PVTILMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNR 240 1 MRITVVLIMKASVIEMPLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEPIV .. 0 100.0%; Score 3502; DB 9; Length 678; 100.0%; Pred. No. 1.7e-293; trive 0; Mismatches 0; Indels 0; R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-66-24
R PELLING DATE: 1998-66-24
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R FILING DATE: 1998-66-24
R APPLICATION NUMBER: 60/09044
R APPLICATION NUMBER: 60/090444
R FILING DATE: 1998-66-24
R APPLICATION NUMBER: 60/090445
R RAPLICATION NUMBER: 60/090445 RETLING DATE: 1998-06-24

RAPPLICATION NUMBER: 60/090472

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RAPLICATION NUMBER: 60/090576

RELING DATE: 1998-06-25

RAPLICATION NUMBER: 60/090676

RELING DATE: 1998-06-25

RAPLICATION NUMBER: 60/090696

RELING DATE: 1998-06-25

RAPLICATION NUMBER: 60/091360

RELING DATE: 1998-06-25

RAPLICATION NUMBER: 60/091360

RELING DATE: 1998-06-25

RAPLICATION NUMBER: 60/091360

RELING DATE: 1998-06-26

RAPLICATION NUMBER: 60/091519

RAPLICATION NUMBER: 60/091519

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RAPLICATION NUMBER: 60/091519

RELING DATE: 1998-07-01

RAPLICATION NUMBER: 60/091519

RELING DATE: 1998-07-01

RAPLICATION NUMBER: 60/091519

RELING DATE: 1998-07-02

RAPLICATION NUMBER: 60/091519

RELING DATE: 1998-07-02 Query Match 100. Best Local Similarity 100. Matches 678; Conservative 61 PRIOR g g ð 요 ઠે ઢ ò

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R FILING DATE: 1997-10-17
R PELING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065311
R FILING DATE: 1997-11-13
R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/066770
R PILING DATE: 1997-11-24
R PILING DATE: 1997-11-24
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R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087607
R APPLICATION NUMBER: 60/087607
R APPLICATION NUMBER: 60/08759
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087759
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R APPLICATION NUMBER: 60/08326

R RELING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088167

R APPLICATION NUMBER: 60/088202

R APPLICATION NUMBER: 60/088202

R APPLICATION NUMBER: 60/088212

R APPLICATION NUMBER: 60/088212

R PILING DATE: 1998-06-05

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R APPLICATION NUMBER: 60/088217

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R APPLICATION NUMBER: 60/088026
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R APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/08881
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 241 PRADPGIQRQDPSGAAFQXFVGADVSLGLVPKEELSTQSLEPVSLGDFNCKIDLSFLIDG 300
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                                                      241 PRADPGIQRODPSGAAFOKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG 300
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730PLC56
CURRENT APPLICATION NUMBER: US/09/989,279
FRIDR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Gerber, Hanspeter
Gerriteen, Mary E.
Goddard, Audrey
Godoweki, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
Pan, James
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR APLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091479
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PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-01
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PRIOR PILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PILING DATE: 1998-07-07 VPRIIONICTEFNSOPRN 678 VPRIIONICTERNSOPRN 678 Best Local Similarity 100. Matches 678; Conservative Н Н 241 241 301 361 361 421 601 61 121 181 181 301 421 481 481 541 601 661 661 Query Match 셤 a 임 ð 엄 õ 8 8 8 8 8 6 8 8 8 8 g 8 8 8 셤 ò È ð

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R APPLICATION NUMBER: 60/089167
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R APPLICATION NUMBER: 60/088217
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R APPLICATION NUMBER: 60/088217
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R APPLICATION NUMBER: 60/088734
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R APPLICATION NUMBER: 60/08874
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
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PILING DATE: 1998-06-17
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FILING DATE: 1998-06-18
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                          CATION NUMBER: 60/088033
                                                                       IPPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
                                               1998-06-04
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CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR PAPLICATION NUMBER: 60/09787
PRIOR PLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
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PRIOR PILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR APPLICATION NUMBER: 60/088028
PRIOR PILING DATE: 1998-06-04
PRIOR PULING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
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PRIOR PILING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR PLING DATE: 1996-02-25
PRIOR APPLICATION NUMBER: 60/075915
PRIOR APPLICATION NUMBER: 60/07910
PRIOR PILING DATE: 1996-03-20
PRIOR PILING DATE: 1996-04-28
PRIOR APPLICATION NUMBER: 60/08322
PRIOR APPLICATION NUMBER: 60/08322
                                     Sequence 179, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
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241 PRADPGIQRQDPSGAAPQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
                                                                                                                                  STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI
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APPLICANT: Than Semin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
PILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
                                                                    PRADPGIQRQDPSGAAPQKPVGADVSLGLVPKEBLSTQSLEPVSLGDPNCKIDLSFLIDG
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Patent No. US20020103125A1
GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
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Eaton, Dan L.
Ferrara, Napoleone
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Gerritsen, Mary E.
Goddard, Audrey
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Napier, Mary A.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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100.0%; Pred. No. 1.7e-293;
ive 0; Mismatches 0;
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R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090696

R APPLICATION NUMBER: 60/090862

R APPLICATION NUMBER: 60/090863

R APPLICATION NUMBER: 60/090863

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091860

R FILING DATE: 1998-01-01

R APPLICATION NUMBER: 60/091860
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R APPLICATION NUMBER: 60/091626
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R APPLICATION NUMBER: 60/091633
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R APPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
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                 R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090429

R PILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090431

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

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R APPLICATION NUMBER: 60/090444

R R APLICATION NUMBER: 60/090445

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R APPLICATION NUMBER: 60/090542

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R APPLICATION NUMBER: 60/090557

R APPLICATION NUMBER: 60/090676

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090678

R FILING DATE: 1998-06-25

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APPLICATION UNMERS: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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Matches 678; Conservative
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PRIOR APPLICATION NUMBER: 60/089512
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PRIOR PLILICADENT NUMBER: 60/089519
PRIOR PLILICADENT NUMBER: 60/089601
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-17
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PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
PRIOR PLING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PPLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
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R APPLICATION NUMBER: 60/090355

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090431

R APPLICATION NUMBER: 60/090444

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090445

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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
LING DATE: 1997-06-16
PLICATION NUMBER: 60/062250
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                                 PVTLMOLLAVTVAVATPTTLPRPSPSAASTTSIPRPGSVGHRSQEMDLWSTATYTSSQNR 240
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                                                                                                                                                                                 PRADPGIQRODPSGAAFQKFVGADVSLGLVPKERLSTQSLEPVSLGDPNCKIDLSFLIDG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 179, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
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Gerriteen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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PRIOR APPLICATION NUMBER: 60/049787
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Eaton, Dan L.
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R APPLICATION NUMBER: 60/089512
R FILING DATE: 1998-06-16
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089518
R FILING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/0896090
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/0896090
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089919
R FILING DATE: 1998-06-19
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PRIOR APPLICATION NUMBER: 60/08675
PRIOR APPLICATION NUMBER: 60/08673
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-18
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PRIOR PILING DATE: 1998-06-19
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R APPLICATION NUMBER: 60/088202
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088212
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
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R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/08873
R FILING DATE: 1998-06-10
                                                    R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R FILING DATE: 1998-06-04

R PILING DATE: 1998-06-04

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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PRIOR PLILOR DATE: 1907-06-16
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PRIOR PLILOR DATE: 1907-11-12
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PRIOR PLILOR DATE: 1907-11-13
PRIOR PLILOR DATE: 1907-11-13
PRIOR PLILOR DATE: 1907-10-17
PRIOR PLILOR DATE: 1908-00-20
PRIOR PLILOR DATE: 1908-00-30
                                                                                                                         Sequence 179, Application US/0990442
Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Pan, James
Paoni, Nicholas F.
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Botstein, David
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PEPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT PILING DATE: 2001-11-14
                                               PVITLMQLLLAVIVAVATPITLPRPSPSAASTISIPRPQSVGHRSQEMDLWSTATYTSSQNR
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Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Goddwaki, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kiljavin, Tvar J.
Napier, Mary A.
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Williams, P. Mickey
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Stewart, Timothy A
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Gerritsen, Mary B.
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Baton, Dan L.
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Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/090359
PRIOR FILING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PRILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
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PRIOR PRILICATION NUMBER: 60/09069
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091696
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-07-07
PRIOR PRIING DATE: 1998-07-07
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NUMBER: 60/049787 1997-06-16 NUMBER: 60/062250 1997-10-17 NUMBER: 60/065186 1997-11-12 NUMBER: 60/065311 1997-11-13 NUMBER: 60/06770 1997-11-24 NUMBER: 60/075945 1998-02-25 NUMBER: 60/075945	NUMBER: 60 1998-04-2) NUMBER: 60 NUMBER: 60 1998-05-0 NUMBER: 60	1998 - 19
APPLICATION FILING DATE: APPLICATION	A CONTRACTOR OF THE CONTRACTOR	
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PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION UNDERE: 60/08512
PRIOR APPLICATION NUMBER: 60/08512
PRIOR APPLICATION NUMBER: 60/08512
PRIOR PLINKS DATE: 1998-06-16
PRIOR PLINKS DATE: 1998-06-16
PRIOR PLINKS DATE: 1998-06-17
PRIOR PLINKS DATE: 1998-06-18
PRIOR PLINKS DATE: 1998-06-19
PRIOR PLINKS DATE: 19

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APPLICANT: Secart, Timothy A. APPLICANT: Secart Timothy A. APPLICANT: Secart Timothy A. APPLICANT: Secart Timothy A. APPLICANT: Secart Timothy A. APPLICANT: Timas, Daniel A. APPLICANT: Timas, Daniel A. APPLICANT: Timas, Daniel A. APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Maranabe, Colin K. APPLICANT: Abang, Semin A. Acids Encoding the Same Prince Pr
                                                                                                                                                        Sequence 179, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary B.
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100.0%; Score 3502; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0;
                                                       PRIOR APPLICATION NUMBER: 60/090863
PRIOR FLING DATE: 1998-66-26
PRIOR PILING DATE: 1998-60-26
PRIOR PILING DATE: 1998-00-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09154
PRIOR PILING DATE: 1998-07-01
PRIOR PRILING DATE: 1998-07-02
PRIOR PRILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PRILICATION NUMBER: 60/091638
PRIOR PILING DATE: 1998-07-07
PRIOR PRILING DATE: 1998-07-07
PRIOR PRILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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R APPLICATION NUMBER: 60/089948

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R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/089948

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R APPLICATION NUMBER: 60/089948

R PILING DATE: 1998-06-19
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R FILING DATE: 1998-06-10

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R APPLICATION NUMBER: 60/088810

R APPLICATION NUMBER: 60/088824

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088865

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088861

R PILING DATE: 1998-06-11

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R APPLICATION NUMBER: 60/089105

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R R FILING DATE: 1998-06-11
                R FILING DATE: 1998-06-04
R PAPLICATION NUMBER: 60/088030
R PILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/08033
R APLICATION NUMBER: 60/08326
R APLICATION NUMBER: 60/08326
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-05
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R PILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090254
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
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PILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
PILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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PILING DATE: 1998-06-10
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088029
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PRIOR
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61 KCPAGCQDPKYHYYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120 121 VQSLSLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180 61 KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120 MRTVVLTMKASVI EMPLVLLVTGVHSNKETAKKI KRPKFTVPQINCDVKAGKI IDPBPIV Gape ö Length 678; Indele 100.0%; Score 3502; DB 9; 100.0%; Pred. No. 1.7e-293; ive 0; Mismatches 0; PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR PPLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-26
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R APPLICATION NUMBER: 60/090355
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090435 Query Match Best Local Similarity 100. Matches 678; Conservative н 셤 ò g 8

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MENT FILING DATE: 2001-11-14

A APPLICATION NUMBER: 60/049787

R FILING DATE: 1997-06-16

R APPLICATION NUMBER: 60/062250

R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065311

R FILING DATE: 1997-11-13

R APPLICATION NUMBER: 60/065311

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R APPLICATION NUMBER: 60/078910

R APPLICATION NUMBER: 60/083322

R FILING DATE: 1998-03-20

R FILING DATE: 1998-04-28

R FILING DATE: 1998-06-08

R PILING DATE: 1998-06-07

R APPLICATION NUMBER: 60/087106

R APPLICATION NUMBER: 60/08706

R APPLICATION NUMBER: 60/08706

R RILING DATE: 1998-06-02

R APPLICATION NUMBER: 60/08759

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R APPLICATION NUMBER: 60/087759

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R APPLICATION NUMBER: 60/087759

R FILING DATE: 1998-06-03

R APPLICATION NUMBER: 60/08827

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R APPLICATION NUMBER: 60/08021

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APPLICATION WUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/075945
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APPLICATION NUMBER: 60/088655
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FILING DATE: 1998-06-11
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301 STSIGKRRFRIQKQLLADVAQALDIGPAGPLAGVVQYGDNPATHFNLKTHTNSRDLKTA1 360
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Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Gurney,Austin L.
Kljavin,Ivar J.
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Gerritsen, Mary B.
Goddard, Audrey
Godowski, Paul J.
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Fong, Sherman
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Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-07-07
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R PILING DATE: 1998-06-10
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R PILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/089105
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
R PILING DATE: 1998-06-18
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R APPLICATION NUMBER: 60/08167

R PILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088217

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R APPLICATION NUMBER: 60/08855

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R PILING DATE: 1998-06-10

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APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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APPLICATION UNDBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
                                          FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/089514
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APPLICANT: Roy, Wargaret Aun
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLCS;
CURRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-24
PRIOR PLILNG DATE: 1998-02-25
                                                                                                                            Sequence 179, Application US/09989721 Patent No. US20020142961A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-03
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/084600
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Gurney, Austin I.
Kljavin, Ivar J.
661 VPRIIQNICTEFNSQPRN 678
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Perrara, Napoleone
Fong, Sherman
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Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Pan, James
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STSIGKRRFRIQKQILADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI 360
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                                                                                                                                                                                                                                                                                301 STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNFATHFNLKTHTNSRDLKTAI
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                                                                                  181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPGSVGHRSQEMDLWSTATYTSSQNR
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Gerber, Hanspeter
Gerter, Hanspeter
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Stewart, Timothy A.
Tumas, Daniel
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Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Botstein, David
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100.0%; Pred. No. 1.7e-293;
iive 0; Mismatches 0;
                          R FILING DATE: 1998-06-22

R FILING DATE: 1998-06-23

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R APPLICATION NUMBER: 60/090355

R APPLICATION NUMBER: 60/090429

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R FILING DATE: 1998-06-24

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R APPLICATION NUMBER: 60/090540

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R APPLICATION NUMBER: 60/090557

R APPLICATION NUMBER: 60/090676

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R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/090690
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R APPLICATION NUMBER: 60/090694
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R APPLICATION NUMBER: 60/09086
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R PILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-02
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R APPLICATION NUMBER: 60/091478
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R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
           APPLICATION NUMBER: 60/090254
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Best Local Similarity 100.
Matches 678; Conservative
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CURRENT APPLICATION NUMBER: US/09/992,598 CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/08/02/
PRIOR APPLICATION NUMBER: 60/08/02/
PRIOR PILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/08/02/
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08/02/
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08/02/
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-05
                                             CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
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R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/075945
R APPLICATION NUMBER: 60/078910
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
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R APPLICATION NUMBER: 60/086810
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R PILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/086824
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088655
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/089738
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APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-11
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FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION WUMBER: 60/08940
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PRIOR PLILING DATE: 1998-06-16
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-18
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PRIOR PLILING DATE: 1998-06-25
PRIOR PLILING DATE: 1998-06-25
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PRIOR PLILING DATE: 1998

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APPLICANT: Wood, WILLIAM I.

APPLICANT: Chang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC6
CURRENT APPLICATION NUMBER: US/09/89,293A
CURRENT PILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-03
                                                                                                                                                         Sequence 179, Application US/09989293A Patent No. US20020177164A1 GENERAL INFORMATION:
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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Gurney, Austin L.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Stewart, Timothy A.
Tumas, Daniel
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Napier, Mary A.
Pan, James
Paoni, Nicholas F.
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Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOSLSLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
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100.0%; Pred. No. 1.7e-293;
tive 0; Mismatches 0;
                     R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090862
R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/090863
R FILING DATE: 1998-06-26
R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-01
R RILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091549
R RILING DATE: 1998-07-02
R PILING DATE: 1998-07-02
R PILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091549
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/09159
R FILING DATE: 1998-07-02
R PILING DATE: 1998-07-02
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PILING DATE: 1998-07-07
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
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Best Local Similarity 100.
    APPLICATION NUMBER:
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CURRENT PELICATION NUMBER: US/09/999,735
CURRENT PELICATION NUMBER: G0/049787
PRIOR PELICATION NUMBER: G0/049787
PRIOR PELILING DATE: 1997-06-16
PRIOR PELLING DATE: 1997-06-16
PRIOR PELLING DATE: 1997-06-17
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1998-02-25
PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1998-02-26
PRIOR PELLING DATE: 1998-02-26
PRIOR PELLING DATE: 1998-02-26
PRIOR PELLING DATE: 1998-02-28
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-06-02
PRIOR PELLING DATE: 1998-06-02
PRIOR PELLING DATE: 1998-06-02
PRIOR PELLING DATE: 1998-06-03
PRIOR PELLING DATE: 1998-06-03
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PRIOR PELLING DATE: 1998-06-05
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RR FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
RR FILING DATE: 1998-06-10
RR APPLICATION NUMBER: 60/088810
RR FILING DATE: 1998-06-10
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PILLING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
FILLING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088826
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FILE REFERENCE: P2730P1C61
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                                                                                                                                                                                                                                                                                                                       EKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVVWYDGWPTDKVERASRLARES 420
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                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                       EKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARES 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDRIACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKKFFISDTDTRIGAVQYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 179, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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R APELICATION NUMBER: 60/089513
R APPLICATION NUMBER: 60/089532
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R APPLICATION NUMBER: 60/089598
R PILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/090246
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R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090354
R FILING DATE: 1998-06-22
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R APPLICATION NUMBER: 60/090431

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R APPLICATION NUMBER: 60/09057

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                                                              R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
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R PILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/089512
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R APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/090695
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KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120 61 KCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNG 120 VOSLSLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPFIPGTTAQ 180 STSIGKBRPRIGKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAI 360 MRTVVI TWIKSVI EMPLVILVTGVHSNKETAKKI KRPKFTVPQI NCDVKAGKI IDPBFIV 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNR PRADPGIQRODPSGAAPQKPVGADVSLGLVPKEBLSTQSLBPVSLGDPNCKIDLSFLIDG MRTVVLTMKASVI EMPLVLLVTGVHSNKETAKKI KRPKFTVPQINCDVKAGKI I DPBPI V TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKBPBISDTDTRIGAVQYT YEORLEPGPDKYSSKPDILMAIKRVGYWSGGTSTGAAINPALEQLFKKSKPNYRKLMILI TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBELBVIATHPARDHSPFVDBPDNLHQY EKI TORGGLSNVGRAI SPVTKNPPSKANGNRSGAPNVVVVMVDGWPTDKVBRASRLARES GINI PPITI BGAAENEKOYVVBPNPANKAVCRTNGFYSLHVQSWFGLHKTLQPLVKRVCD Gaps ö Length 678; 0; Indels 100.0%; Score 3502; DB 9; 100.0%; Pred. No. 1.7e-293; ive 0; Mismatches 0; R PILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090696
R PILING DATE: 1998-06-25
R PILING DATE: 1998-06-26
R PILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/090863
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R APPLICATION NUMBER: 60/091860
R PILING DATE: 1998-06-26
R PILING DATE: 1998-07-01 R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-01
R PILING DATE: 1998-07-02
R PILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
R FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-09 Query Match Best Local Similarity 100.8 Matches 678; Conservative 241 1 61 121 181 241 301 361 541 301 361 421 421 601 481 PRIOR ò 셤 è 쉽 õ g 셤 ò a ò 용 ठे 셤 ठे 셤 Š 욢 ð 8

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601 TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBELEVIATHPARDHSFPVDBFDNLHQY

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Search completed: May 27, 2004, 16:49:26 Job time : 64 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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OM protein - protein search, using sw model

May 27, 2004, 16:41:07 ; Search time 22 Seconds (without alignments) 1604.708 Million cell updates/sec Run on:

Pitle:
Perfect score:

US-10-063-688-34 3502 1 MRTVVLTMAGASVIEMFLVLL......QYVPRIIQNICTEFNSQPRN 678

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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POTENTIAL.

Glycoprotein; Repeat; Signal SIGNAL 1

Pfam; PF03815; LCCL; 1.
Pfam; PF00092; vwa; 2.
PRINTS; PR00453; VWRADOWAIN.
SMART; SM00603; LCCL; 1.
SMART; SM00327; VWA; 2.
PROSITE; PS50820; LCCL; 1.

Q28902 oryctolagus P15988 gallus gall P20701 homo sapien Q02701 88 mus musculu P18614 rattus norv P12110 homo sapien P24063 mus musculu P56199 homo sapien Q901x5 homo sapien Q90615 gallus gall P53710 homo sapien P17301 homo sapien	
CAIC_RABIT CA26_CHICK ITAL HUMAN CA26_MOUSB ITAL RAT CA26_HUMAN ITAL_HUMAN ITAL_HUMAN ITAL_CHICK ITAL_CHICK ITAL_CHICK	
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211.5 209.5 207.5 203.5 203.5 200.1 195 192.5 188.5 187.5	
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                               Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                           NOTE-Issue 4 of November 2000;
WWW="http://www.expasy.org/spotlight/articles/sptlt004.html".
                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
COCH ON COCHSB2.
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InterPro; IPR004043; LCCL dom.
InterPro; IPR002035; VWF_A.
          STANDARD:
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         COCH CHICK
COCH CHICK
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disorder."
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                                                                                                                                                                                                                                                                                                                                                             VLCPANCPLWQFYVPGDGIYASLSSVCGAAIHRGVITNAGGAVRVQTLPGQENYPAVHAN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||: | :: || ||: ||: ||: ||: ||: |||| ||: |||| ||: |||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||: ||| ||| ||: ||| ||: ||| ||: ||| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVQSLSLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIQSQVLSRWASSFSV----TPGTNN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 QPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 RPRADPGIQRQDPSGAAPQKPVGADVSLGLVPKEELSTQSLRPVSLGDPNCKIDLSFLID 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSTSIGKRRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGINIPPITIEGAAENEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLQPLVKRVC 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I EXI TORGGLSNVGRAISFVTKNPPSKANGNRSGAPNVVVVNVNVDGWPIDKVERASRLARB
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                                                                                                                                                  .) (POTENTIAL)
                                                                                                                                                                                                                                                     Best Local Similarity 37.3%; Pred. No. 2.8e-67;
Matches 229; Conservative 104; Mismatches 165; Indels 116;
                                                                                                                                                                                                                           Length 547;
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59426 MW; 172724242641DF88 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
15-MAY-2004 (Rel. 43, Last annotation update)
15-COCHIN precursor (COCH-5B2) (UNQ257/PRO294).
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MEDLINE=21458424; PubMed=11574466;
Liepinsh B., Trexler M., Kaikkonen A., Weigelt J., Banyai L.,
Patthy L., Otting G.;
"NMR structure of the LCCL domain and implications for DPNA9 deafness
MEDLINE-98110569; PubMed-9441737; Robertson N.G., Skvorak A.B., Yin Y., Weremowicz S., Johnson K.R., Kovatch K.A., Battey J.F., Bieber F.R., Morton C.C.; "Mapping and characterization of a novel cochlear gene in human and imouse: a positional candidate gene for a deafness disorder, DFNA9."; Genomics 46:345-354 (1997).
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                                                                                                                                                                                                                                                                                                                                                                        Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J., Chen J., Clow B., Crowley C., Currell B., Douel B., Dowd P. Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Kilmowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Watead D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-22727166; PubMed=12843317;
Robertson N.G., Hamaker S.A., Patriub V., Aster J.C., Morton C.C.;
"Subcellular localisation, secretion, and post-translational
processing of normal cochlin, and of mutants causing the
sensorineuxal deafness and vestibular disorder, DRNA9.";
J. Med. Genet. 40:479-486 (2003).
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MEDLINE=21193177; PubMed=11295836;
Kamarinos M., McGill J., Lynch M., Dahl H.-H.M.;
"Identification of a novel COCH mutation, I109M, highlights the similar clinical features observed in DFNA9 families.";
Hum. Mutat. 17:351-351(2001).
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Hum. Mutat. 18:547-548(2001).
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VARIANT DFNA9 THR-119.
MEDLINB=22873884; PubMed=14512963;
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and the vestibule.

-!- PTM: N-glycosylated.
-!- PTM: A 50 kDa form is created by proteolytic cleavage.
-!- PTM: A 50 kDa form is created by proteolytic cleavage.
-!- PTM: A 50 kDa form is created by proteolytic cleavage.
-!- PTM: A 50 kDa form is created by proteolytic cleavage.
-!- DISEASE: Defects in COCH are the cause of autosomal dominant nonsyndromic sensorineural deafness type 9 (DFNA9) [MIN:601369].
-!- Hearing loss begins in the fourth or fifth decade of life and initially involves the high frequencies. Deafness is progressive and usually complete by the sixth decade. In addition to cochlear involvement, DFNA9 patients also exhibit a spectrum of vestibular dysfunctions. Penetrance of the vestibular symptom is often incomplete, and some patients are minimally affected, whereas others suffer from severe balance disturbances and episodes of vertigo. Affected individuals have mucopolysaccharide depositions in the channels of the cochlear and vestibular nerves. These depositions apparently cause strangulation and degeneration of dendritic fibers. Usami S., Takahashi K., Yuge I., Ohtsuka A., Namba A., Abe S., Fransen E., Patthy L., Ottling G., Van Camp G.; Partiations in the COCH gene are a frequent cause of autosomal dominant progressive cochleo-vestibular dysfunction, but not of Meniere's extracellular matrix. -!- TISSUB SPECIFICITY: Expressed in inner ear structures; the cochlea HARACTERIZATION OF VARIANTS DFNA9 SER-51; GLY-66; GLU-88; ASN-109 AND "Mucations in COCH that result in non-syndromic autosomal dominant deafness (DFNA9) affect matrix deposition of cochlin.";

Hum. Genet. 113:406-416(2003).

-1- SUBCELLULAR LOCATION: Extracellular. Associated with the ARG-117. MEDLINE=22866968, PubMed=12928864; Grabski R., Szul T., Sasaki T., Timpl R., Mayne R., Hicks B. Bur. J. Hum. Genet. 11:744-748(2003).
[10]

SIMILARITY: Contains 1 LCCL domain.
SIMILARITY: Contains 2 VWFA domains.
DATABASE: NAME=Protein Spotlight;
NOTE=Issue 4 of Novers 2000;
WWW=http://www.expasy.org/spotlight/articles/sptlt004.html*.
DATABASE: NAME=Hereditary hearing loss homepage; NOTE=Gene page; WWW="http://www.uia.ac.be/dnalab/hhh/"

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R InterPro; IPR004043; LCCL_dom.
R InterPro; IPR002035; VWP_A.
R Pfam; PP030915; LCCL; 1.
R PRINTS; PR00453; VWFADOWAIN.
R SMART; SM00603; LCCL; 1.
R SMART; SM0037; VWFA, 2.
R PROSITE; PS50820; LCCL; 1.
R PROSITE; PS50820; LCCL; 1.
R PROSITE; PS50820; LCCL; 1.
R PROSITE; PS50834; VWFA; 2.
R Glycoprotein; Repeat; Signal; Disease mutation; Deafness; POLYMORPHISM: 3D-structure.
R SIGNAL EMBL; AF006740; AAC39545.1; -.
EMBL; AY35800; AAQ89259.1; -.
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m				-	-	-	(*)		Ï	INCDVKAGKIIDPEPIVKCPAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKIL 	VRKVAGQSGYKGSYSNGVQSLSLPRWRBSPIVLRSKPKKGVTYPSALTYSSSKSPAAQAG	VYSLPGRENÝSSVDANGIQSQMLSRWSASFTVTKGK	BTTKAYQRPPI PGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSI PRPQSVGHRS :		QEMDLWSTATYTSSQNRPRADPGIQRQDPSGAARQKPVGADVSLGLVPKBELSTQSLEPV : : ::: PRTRIKKTPRKK	SLGI	:: :: : : : - : - : - : - :- :-	HFNLKTHTNSRDLKTALEKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVMVD 	GWPTDKVEBASRLARESGINI PFITIBGAAENEKQYVVEPNFANKAVCRTNGFYSLHVQS		WPGIHKTLOPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNPRTVLOPVTNLTK	WPG:	EFEISDIDTRIGAVOTTYBORLERGEDEKYSSKEDILNAIKRYGYWSGGISTGAAINFALK
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X REDLINE=22388257; PubMed=12477932;

A Straueberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Klauener R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,

A Lischul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gluba R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.B.,

"Generation and initial analysis of more than 15,000 full-length
 584 OLFK--KSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIAT 641
                 MEDLINE=97237053; PubMed=9119401;
A Crozet F., Amraoui A.B., Blanchard S., Lenoir M., Ripoll C., Vago P.,
Crozet F., Amraoui A.B., Blanchard S., Lenoir M., Ripoll C., Vago P.,
A Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattei M.-G.,
A Weil D., Pujol R., Petit C.;
I "Cloning of the genes encoding two murine and human cochlear
unconventional type I myosins.";
Genomics 40:332-341(1997).
C -! SIBCELPICITY: Expressed in inner ear structures.
C -! SIMILARITY: Contains 1 LCCL domain.
C -! SIMILARITY: Contains 2 VWFA domains.
C -! SIMILARITY: Contains 2 VWFA domains.
C -! SIMILARITY: Contains 2 WFA domains.
C -! MYTRALESUE 4 Of November 2000;
WWW="http://www.expasy.org/spotlight/articles/sptlt004.html".
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98110569; PubMed=9441737; Robertson N.G., Skvorak A.B., Yin Y., Weremowicz S., Johnson K.R., Kobertson N.G., Battey J.P., Bieber F.R., Morton C.C.; "Mapping and characterization of a novel cochlear gene in human and imouse: a positional candidate gene for a deafness disorder, DFNA9."; Genomics 46:345-354(1997).
                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                COCH MOUSE STANDARD; PRT; 552 AA. 062507; Q9QWK6; 30-MAY-2000 (Rel. 39, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last amoutation update) Cochlin precursor (COCH-5B2).
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                                                                                         545
                                                             642 HPARDHSFFVDEFDNLHQYVPRIIQNICTEF
                                                                                      515 KPKESHAPPTREPTGLEPIVSDVIRGICRDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 131.8%; Score 1113; DB 1; Length 552; Local Similarity 36.2%; Pred. No. 1.4e-65; les 233; Conservative 105; Mismatches 185; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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LCCL.
VWFA 1.
VWFA 2.
BY SIMILARITY.
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InterPro; IPR002035; VWF A.
Pfam; PP003815; LCCL; 1.
Pfam; PP00902; VWa; 2.
PRINTS; PR00453; VWa, DARADOMAIN.
SWART; SM00603; LCCL; 1.
                                                                                                                                                                                                                             EMBL; AF006741; AAC39949.1; -.
                                                                                                                                                                                                                                                 BC045137; AAH45137.1; -. Z78163; CAB01565.1; -. P11215; 1JIM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50820; LCCL; 1.
PROSITE; PS50234; VWPA; 2.
                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1278313; Coch.
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629
                                                           Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H., Nishida Y., Obara M., Kimata K.; Inshida Y., Obara M., Inshida Y., Obara 
                               TSTGAAINPALEQLFK--KSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95370352; PubMed=7642694;
Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
"Large and small splice variants of collagen XII: differential
expression and ligand binding.";
J. Cell Biol. 130:1005-1014(1995).
-!- FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COLI domain could be associated with the
surface of the fibrils, and the COLI and NC3 domains may be
localized in the perifibrillar matrix.
-!- SUBUNIT: Trimer of identical chains each containing 190 kba of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R., Type XII collagen. A large multidomain molecule with partial homology to type IX collagen. †
J. Biol. Chem. 264:19772-19778(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Embryo;
MEDLINE=93042014; PubMed=1420368;
Trueb J., Trueb B.;
Trueb B.;
Trueb B.;
Trueb B.;
Biochim. Biophys. Acta 1171:97-98(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-87317590; PubMed-3476925;
Gordon M.K., Gerecke D.R., Olsen B.R.;
"Type XII collagen: distinct extracellular matrix component
discovered by cDNA cloning.";
                                                                                                                                               630 WAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEF 672
                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(XII) chain precursor (Fibrochimerin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=White leghorn;
MEDLINE=92011862; PubMed=1918137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EDLINE=90062079; PubMed=2584192;
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01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 2960-3076 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or any
combination of isoform Long and isoform Short. Only isoform
is a proteoglycan. Isoform Long has more restricted expression
in embryonic tissue than isoform Short;
                                                                                                                                                                                                                                                                                                                                                                                        -I- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                      ISOIGEP13944-2; Sequence=VSP 001148;
ISOIGEP13944-2; Sequence=VSP 001148;
IISOIGE SPECIFICITY: Type XII collagen is present in tendons,
ligaments, perichondrium, and periosteum, all dense connective
tissues containing type I collagen.
DOWAIN: This sequence defines five distinct domains, two triple-
helical domains (COL1 and COL2) and three nontriple-helical
domains (NCI, NCZ, and NC3).
PTM: The triple-helical tail is stabilized by disulfide bonds at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -|- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELLCES (FACIT) FAMILY.
-|- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
-|- SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 18 fibronectin type III domains.
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COLLAGEN ALPHA 1(XII) CHAIN.
FIBRONECTIN TYPE-III 1.
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FIBRONECTIN TYPE-III
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PIBRONECTIN TYPE-III
PIBRONECTIN TYPE-III
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                                                                                                                                                    IsoId=P13944-1; Sequence=Displayed;
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416 TIMEKTQQVKV-----QVECSRGVDVKADVVFLVDGSYSIGIAMFVKVRAFLEVLVKS 468
                                                                  AND XIB-2).

C. STRAIN-C57BL/GJ. TISSUB-SKIN fibroblast;

MEDLINE-99148349; PubMed=10419532;

Kania A.M., Reichenberger B., Baur S.T., Karimbux N.Y., Taylor R.W.,

A Olsen B.R., Nishimura I.;

Gleen B.R., Nishimura I.;

Structural variation of type XII collagen at its carboxyl-terminal

To Structural variation of type XII collagen at its carboxyl-terminal

WC1 domain generated by tissue-specific alternative splicing.*;

J. Biol. Chem. 274:22053-22059(1999).

J. Biol. Chem. 274:22053-22059(1999).

Containing fibrils, the CC01 domain could be associated with the surface of the fibrils, and the CC02 and NC3 domains may be localized in the perfifbrillar matrix (By similarity).

Containing spoucras sequences (By similarity).

C.I. ALTERNATIVE PRODUCTS:

Comment-Alternative Splicing; Named isoforms=4;

Comment-The final tissue form of collagen XII may contain homotrimers or any combination of the various isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOId-60047-4; Sequence=VSP 001150, VSP 001151, VSP 001152; ISOId-60047-4; Sequence=VSP 001150, VSP 001151, VSP 001152; TISSUB SPRCIPICITY: Highest expression in tendons, perichondrium, skin, cornea, sclera, blood vessels, and periosteum. DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are predominant at early stages (ED7 and 11); at later stages of development (BD15 and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major forms are the short NC3 forms become the wajor product, the long splice variant
                                                                                                            585 LP---KKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBBLBVIAT
                                                                                                                            PEISDTDTRIGAVQYTYEORLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Swiss Webster, and C57BL/6J; TISSUE=Skin; MEDLINE=96170761; PubMed=8601036; MEDLINE=96170761; Oh P.S., Olleen B.R.; Popperary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic
                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=XIIA-2; Synonyms=ER#K;
IsoId=Q60847-2; Sequence=VSP_001151, VSP_001152;
                                                                                                                                                                                         HPARDHSPFVDEFDNIHQYVPRIIQNICTEFNSQ 675
                                                                                                                                                                                                                                                                                 CAIC_MOUSE STANDARD; PRT; 3119 AA. Q60847; P70322; 15-JUL-1998 (Rel. 36, Created) 28-FRE-2003 (Rel. 41, Last sequence update) Collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q60847-3; Sequence=VSP_001150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold=Q60847-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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TRIPLE-HELICAL REGION
(NCL1) WITH 2 INPERFECTIONS.
NONHELICAL REGION (NC1).
ASP/GLU-RICH (ACIDIC).
ARG/LYS-RICH (BASIC).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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NONHELICAL REGION (NC3).
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(COL2) WITH 1 IMPERFECTION.
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-> B (IN RBF. 4).
-> A (IN RBF. 2).
-> F (IN RBF. 2).
-> F (IN RBF. 2).
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Pred. No. 8.5e-28;
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                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:88448; Coll221.

R InterPro; IPR001816; Collagen.

R InterPro; IPR001857; FW III-like.

InterPro; IPR001359; FW III-like.

R InterPro; IPR001329; TSPN.

R InterPro; IPR001329; TSPN.

R InterPro; IPR001319; TSPN.

R Pfam; PP01391; Collagen; 5.

R Pfam; PP01391; Collagen; 5.

R Pfam; PP00210; TSPN; 1.

R PRINTS; PR00453; VWFADOMAIN.

R PRINTS; PR00453; VWFADOMAIN.

R SMART; SM00020; TSPN; 1.

R SMART; SM00221; TSPN; 1.

R SMART; SM00227; VWR; 4.

R PROSTTE; PS50234; VWR; 4.

R RATACCEllular matrix; Connective tissue; Repeat; Hydroxylation; Collagen; Signal; Glycoprotein; Alternative splicing.

T SIGNAL
-!- FTM: O-glycosylation of isoform XIIA-2; glycosaminoglycan of chondroitin-sulfate type (By similarity)
-!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FAMILY.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
-!- SIMILARITY: Contains 4 WWPA domains.
-!- SIMILARITY: Contains 18 fibronectin type III domains.
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TRIPLE-HELICAL REGION
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EMBL; U57095; AAB07047.1; -.
HSSP; P02751; 1FNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> GSG (in isoform XIIA-2 and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
O-LINKED (XYL. . .) (CHONDROITIN SULPATE)
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O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
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(POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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15.8%; Score 552; DB 1; Length 3119;
Best Local Similarity 27.5%; Pred. No. 1.1e-27;
Matches 174; Conservative 77; Mismatches 209; Indels 172; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 SLEPVSLGDPNCKI----DLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGV
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
Missing (in isoform XIIB-) and isoform
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NOWHELICAL REGION (NC2).

TRIPLE-HELICAL REGION
(CCLL) WITH 2 IMPERFECTIONS.

NOWHELICAL REGION (NC1).

CELL ATTACHMENT SITE (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
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3119 AA; 340239 MW; 9B1F999C86AB3251 CRC64;
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TOPKTQPMKVQV-----ECSRGVDIKADIVFLVDGSYSIGTAMPVKVRAFLEVLAKSFE 475
     ------HK 469
                                                      362 TGYKILLTPMAAGSRHHALSVGPOTTTLNVRDLTADTEYQISVFAMKGLTSSEPTSVMEK 421
                                                                                                                                                                                                                                                                                                                                 ---KKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHP 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.

MEDLINE=97288521; PubMed=9143499;
Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.;
T. Complete primary structure of two splice variants of collagen XII,
and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX)
collagen (COL9A1), and alpha 1(XIX) collagen (COL12A1), alpha 1(IX)
collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human
chromosome 6q12-q13."

Genomics 41:236-242(1997).

Celecke A1:236-242(1997).

Containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).

Celecke Demonstration of alpha 1(XIX) collagen containing 190 kDa of incertiple-relacal chains each containing 190 kDa of containing 19
                                                                                                                                                                                                                                                 T---LOPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFB
                                                                                                                                                                                                                  ISDIDTRIGAVQYTYBQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINPALEQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoid=099715-2; Sequence=VSP 001149; TISSUE SPECIFICITY: Found in collagen I-containing tissues: both short and long isoforms appear in ammion, chorion, skeletal mascle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the short isoform is found in lung, placenta, kidney and a squamous cell carcinoma cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).

PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATION PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment-The final tissue form of collagen XII may contain
Comment-The final issue form of collagen XII may contain
homocrimers of either isoform Long or isoform Short or any
combination of isoform Long and isoform Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: O-glycosylation of isoform Long; glycosaminoglycan of chondroitin-sulfate type (By similarity).
SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
  ----XSLHVQSWPGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALCHUMAN

CALCHUMAN

CALCHUMAN

TO CALC HUMAN

TO CALC HUMAN

TO S-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 34) Last annotation update)

DT 15-JUL-1998 (Rel. 34) Last sequence update)

DT 15-JUL-1998 (Rel. 34) Last sequence update)

COL12AAL

COL12AAL

SULPAR-2004 (Rel. 43) Last annotation update)

COL12AAL

HOMEN SAPINE STANDAND (ACCORDAN CARNIGAL OF ACCORDAN CARNIGATION COMPLET PRESSOR (ACCORDAN CARNIGATION CARNIGATION COMPLET PRESSOR (ACCORDAN CARNIGATION CARNIGATION CARNIGATION CARNIGATION COMPLETE PRIMARY STRUCTURE OF (WO SPILICE VARIAN)

REDITES 7288251, PUMBACE 914389;

RA GRECKE D.R., Olson P.E., Koch M., Knoll J.H.M., RA GRECKE D.R., Olson P.E., Koch M., And alpha 1(XIX) Collagen (COL12AN)

RY GROOMS (COL12AN), and alpha 1(XIX) Collagen (COL12AN)

RY CALCHOROSOME 66412-413.";

GENOMICS 41:236-242(1997)

CC CONTAINING fibrils, the COL1 domain could be surface of the fibrils, and the COL2 and NC3 (COMPANIAN) and sequences.

CC ALTERNATIVE PRODUCTS:

CC COMMANIANT PRESSOURCES:

CC COMMANIANT PRESSOURCES:

CC ALTERNATIVE PRODUCTS:

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CC COMPANIANT PRESSOURCES AND SOCIARDS AND SOCIARD SOCIARD AND SOCIARD                                                                                                                                                                                                                                                                                                                                                                                                                                              ARDHSFFVDRFDNLHQYVPRIIQNICTEFNSQ 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFIAM; PP00092; vwa; w. PRINTS, PROMESS; www.p. PRINTS; PROMESS; www.p. PRINTS; PROMESS; www.p. Marker; SM00060; FYSPN; 16.
SWART; SM00210; TSPN; 1.
SWART; SM00217; VWA; 4.
PROSITE; PS50234; VWPA; 4.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
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(COLI) WITH 2 IMPERFECTIONS.
(COLI) WITH 2 IMPERFECTIONS.
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLLAGEN ALPHA 1 (XII) CHAIN, PIBRONECTIN TYPE-III 1.
NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION
(COL2) WITH 1 IMPERPECTION.
NONHELICAL REGION (NC2).
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PIBRONBCTIN TYPE-III 19
PIBRONBCTIN TYPE-III 19
PIBRONBCTIN TYPE-III 11
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FIBRONECTIN TYPE-III
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PIBRONECTIN TYPE-III
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                                                                                                                                                                                                                                                                                                                    GO; GO:0005595; C:collagen type XII; TAS.
GO; GO:0001501; P:skeletal development; TAS.
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InterPro; IPR008957; FW III-like.
InterPro; IPR008957; FW III.
InterPro; IPR00129; TSPN.
InterPro; IPR002035; VWF.A.
Pfam; PP01391; Collagen; 4.
Pfam; PP02010; TSPN; 1.
Pfam; PP02010; TSPN; 1.
                                                                                                                                                                                                                            EMBL; U73778; AAC51244.1; -. EMBL; U73779; AAD40483.1; -. HSSP; P02751; ITTF.
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MIM; 120320; -.
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(XYL. . .) (CHONDROITIN SULPATE)
                                                                                                                                                                                                                                                                                                             179 AQPVTLMQLLAVTVAVATPTTLPRPSPS-----AASTTS-----IPRPQSVGHRSQEMD
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
Missing (in isoform Short).
                                                                                                                                                                                                                                                                    15.5%; Score 543.5; DB 1; Length 3063; 27.7%; Pred. No. 4e-27; Live 76; Mismatches 207; Indels 165;
                                                                                                                    (POTENTIAL)
                                     SIMILARITY).
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N-LINKED (GLCNAC.
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Matches 172; Conservative
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2206
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                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeating
                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                            MEDIJUR=90212613; PubMed=2322559;
Bonaldo P., Russo V., Bucciotti F., Doliana R., Colombatti A.;
Structural and functional features of the alpha 3 chain indicate
bridging role for chicken collagen VI in connective tissues.";
Biochemistry 29:1245-1254 (1990).
                                                                                                                                                                                                   MEDLINE=91035630; PubMed=1977751;
Doliana R., Bonaldo P., Colombatti A.;
Multiple forms of chicken alpha 3(VI) collagen chain generated alternative splicing in type A repeated domains.";
J. Cell Biol. 111:2197-2205(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bvent=Alternative splicing; Named isoforms=1;
Comment=At least 2 isoforms are produced;
                                  01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
         PRT; 3137 AA
                                                                        Collagen alpha 3(VI) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P1211; ZKNT.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; ClJ dgen.
InterPro; IPR008361; FN III.
InterPro; IPR002223; Kumitz_BPTI.
InterPro; IPR002235; WWP_A.
Pfam; PP01391; Collagen; 6.
Pfam; PP00041; fin3; 1.
Pfam; PP00014; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                                                                       SEQUENCE OF 224-2871 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M24282; AAA03201.1; -.
                                                                                                                                                                                SEQUENCE OF 1-853 FROM N.A.
          STANDARD;
                                                                                                   Sallus gallus (Chicken)
                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                            TISSUE=Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1;
          GHICK
                    P15989;
                                                                                                                                           Gallus
CA36_CHICK
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LEQLEKKSKENK-----RKCMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBBL 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM: 115437; -. Gextracellular matrix; TAS. GO; GO:0005578; C:extracellular matrix structural constituent; TAS. GO; GO:0005201; P:extracellular matrix structural constituent; TAS. GO; GO:0006461; P:protein complex assembly; TAS. InterPro; IPR006210; EGF like. InterPro; IPR006210; EGF. InterPro; IPR006210; EGF. InterPro; IPR002035; VWP.A.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-91060568; PubMed=2246248;
MEDLINE-91060568; PubMed=2246248;
MEDLINE-91060568; PubMed=2246248;
Byers M.G., Shows T.B., Duby A.D.;
"Structure and chromosomal location of the human gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      component of the
                                                                                                                                                                                                                                                                                                                                              Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage matrix protein.";
J. Biol. Chem. 265:19624-19631(1990).
-!- FUNCTION: Cartilage matrix protein is a major component o extracellular matrix of nonarticular cartilage. It binds
                                                                                                             668
                                                                                                                                          418
                                                                                                                                                                                                                                                    01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cartilage matrix protein precursor (Matrilin-1)
MATNI OR CRYP OR CMP.
Homo sapiens (Human).
                                                                                                                                QOIAT----DGSFAFTALDIRNLAALRELLLPNI
                                                                                                             EVIATHPARDHSPPVDEPD--NLHQYVPRIIQNI
                                                                                                                                                                                                                        496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Homotrimer.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 2 VWPA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00008; EGF; 1.
Pfam; PF00092; vwa; 2.
PRINTS; PR00453; VWFADONAIN.
SMART; SMO0181; EGF; 1.
SMART; SM00127; VWA; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; NSS675; AAB38702.1; JOINED.
EMBL; MSS676; AAB38702.1; JOINED.
EMBL; MSS677; AAB38702.1; JOINED.
EMBL; MSS680; AAB38702.1; JOINED.
EMBL; MSS680; AAB38702.1; JOINED.
EMBL; MSS681; AAB38702.1; JOINED.
EMBL; MSS683; AAB38702.1; JOINED.
EMBL; MSS683; AAB38702.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M55682; AAB38702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSBP; PO5099; 1AO5.
Genew; HGNC:6907; MATNI.
MIM; 115437; -.
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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P21941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPSSVIKSAHVNMIAVGVQDAVEGELKEIASRPFDT-----HIFNLENFTALHGI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 KEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDIIMAIKRVGYWSG-GTSTGAAINPA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R PFIMIS; PR0092; vwa; 11.

R PRINTS; PR00159; BASICFTASE.

R PRINTS; PR0016453; VWFADOMAIN.

R PRODOM; PD001007; C1g, helix; 1.

R SMART; SM00122; Kunitz_BPT1; 1.

R SMART; SM00131; Kuj; 1.

R PROSITE; PS00280; BPTT KUNITZ_1; 1.

R PROSITE; PS50229; BPTT KUNITZ_2; 1.

R PROSITE; PS50224; VWFP; 12.

R PROSITE; PS50224; VWFP; 12.

R PROSITE; PS50224; VWFP; 12.

M Extracellular matrix; Connective tissue; Repeat; Hydroxylation; M Glycoptetin, Cell adhesion; Serine protease inhibitor; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIIPLVDSSWSIGKEHPQLVREFLYDVVKALDVGGNDFRPALVQFSGNPHTEPQLNTYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 SRDLKTAIEKITORGGLSNVGRAISFVTKNPFSKANGNRS--GAPNVVVMVDGWPTDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOPLUK--RUCDTDRLACSK----TCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLT
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FIRRONECTIN TYPE-III.

RPITTKONITZ INHIBITON.

INTERRUPTION IN COLLAGENOUS REGION.

INTERRUPTION IN COLLAGENOUS REGION.

CELL ATTACHMENT SITE.

REACTIVE BOND (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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AA; 339595 MW; ECB428578B536357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87; Mismatches 155; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 504.5; DB 1; Length 3137; Pred. No. 1.5e-24;
                                                                                                                                                                                                                                    COLLAGEN ALPHA 3 (VI) CHAIN.
NONHELLICAL REGION.
TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC. . . .
                                                                                                                                                                                                                                                                                     NONHELICAL REGION.
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                                                                                                                                                                                                                       POTENTIAL
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N-LINKED
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VWFA 2.
VWFA 4.
VWFA 5.
VWFA 5.
VWFA 6.
VWFA 7.
VWFA 7.
VWFA 1.
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2172
2259
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                                                                                                                                                                                                                                                                                                                                                                                    330 PLMGVVQYGDNPATHFNLKTHTNSRDLKTAIBKITQRGCLSNVGRAISFVTKNPFSKANG 389
                                                                                                                                                                                                                                                                                                                                                                                                                    137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : : | : | : | : | : | : | 107 DEHVD------YVESYSVIEKLSRKFQEAFCVVSDLCATGDHDCEQVCISSPGSYT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 NRSGAPN---VVVVMVDGWPTDKVBEASRLARESGINIPFITIEGAAENE--KQYVVEPN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 FANKAVCRTNGFYSLHVQSWFGLHKTLQP-----LVKRVCDTDRLACSKTCLNS---- 493
                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                     367 TVSSGARPGAQKVGIVFTDGRSQDYINDAAKKAKDLGFKMFAVGVGNAVEDELRBIASEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 -----ADIGEVIDGSSSVGTGNFRTVLQFVTNLTKEFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                   14.3%; Score 501.5; DB 1; Length 496; 28.8%; Pred. No. 1.6e-25; ative 80; Mismatches 178; Indels 61;
                                                       WFA 1.

BGF-LIKE.

VORA 2.

VORA 2.

VORB 2.

N-LINKED (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=White leghorn;
MEDLINE=8925546; PubMed=2542265;
Kiss I., Deak F., Holloway R.G. Jr., Delius H., Mebust K.A.,
Frimberger E., Argraves W.S., Tsonis P.A., Winterbottom N.,
        EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil.
SIGNAL 1 22
                                                                                                                                                                                                                     2D880A8114C7940F CRC64;
                                             CARTILAGE MATRIX PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1991 (Rel. 18, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Cartilage matrix protein precursor (Matrilin-1)
                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
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                                                                                                                                                                                                                       53700 MW;
                                                                                                                                                                                                                                                                      Best Local Similarity 28.8%
Matches 129; Conservative
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PS50234;
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NCBI_TaxID=9031;
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CARBOHYD
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SEQUENCE
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PROSITE;
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PROSITE; PS00022; EGP 1; PALSE NEG.
PROSITE; PS01186; EGP 2; 1.
PROSITE; PS50234; VWFA; 2.
                                                                                         EMBL; U35035; AAB06521.1; -. PIR; S66522; S66522.
                                                                                                                                                                                                                                                                                PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00181; BGF; 1.
SMART; SM00327; VWA; 2.
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                                                                                                                                                                          293 DLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTN 352
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                                                                                                                                                                                                                                                        353 SRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGNRSGAPN---VVVVMVDGWPTDK 409
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STRAIN=CSPBL/6 X CBA; TISSUB=Cartilage;
MEDLINE=96270751; PubMed=8665920;
Aszodi A., Hauser N., Studer D., Paulsson M., Hiripi L., Bosze Z
Aszodi A., Fauser N., Studer D., Paulsson M., Miripi L., Bosze Z
"Cloning, sequencing and expression analysis of mouse cartilage
                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matrix protein cDNA.";

Rur. J. Biochem. 236.970.997(1996).

-!- FUNCTION: Cartilage matrix protein is a major component o
extracellular matrix of nonarticular cartilage. It binds
                                                                                             Length 493;
                                                                                                                                        68; Mismatches 177; Indels
                                                             54034 MW; E4D3DACFAB2B96A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cartilage matrix protein precursor (Matrilln-1)
MATNI OR CRTM OR CMP.
                                                                                                 Score 490; DB 1;
Pred. No. 9.2e-25;
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29.6%;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28.8%; Pred. No. 9.4e-25;
ive 72; Mismatches 184; Indels
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MGD, MGI:L06591; Matn1.
GO; GO:0005579; C:extracellular matrix; IDA.
InterPro; IPR065209; BGF like.
InterPro; IPR06210; IBGF.
InterPro; IPR00201; IRGF.
Pfam; PF00008; BGF; 1.
Pfam; PF000092; vwa; 2.
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PDB; 1KUN;
PDB; 1KTH;
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SECURENCE OF 32-236 FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=93054780; PubMed=1339440;
Zanussi S., Doliana R., Segat D., Bonaldo P., Colombatti A.;
"The human type VI collagen gene. mRNA and protein variants of the alpha 3 chain generated by alternative splicing of an additional 5-end exon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95182468; PubMed=7533217;
Arnoux B., Merigeau K., Saludjian P., Norris F., Norris K., Bjoern S., Olsen O., Petersen L., Ducruix A.;
"The 1.6 A structure of Kunitz-type domain from the alpha 3 chain of human type VI collagen.";
J. Mol. Biol. 246:609-617(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2092-2157 FROM N.A.
MEDLINE=88029444; PubMed=3665927;
Chu M.-L., Mann K., Deutzmann R., Pribula-Conway D.,
Hsu-Chen C.-C., Bernard M.P., Timpl R.;
"Characterization of three constituent chains of collagen type VI by peptide sequences and cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 3102-3164.
MEDLINE-96398604; PubMed-8805527;
Zweckstetter M., Czisch M., Mayer U., Chu M.-L., Zinth W., Timpl R.,
                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=90151612; PubMed=1689238; Chu M.-L., Zhang R.-Z., Pan T.-C., Stokes D., Conway D., Kuo H.-J., Chu M.-L., Zhang R.-Z., Pan T.-C., Deutzmann R., Timpl R.; Mayer U., Mann K., Deutzmann R., Timpl R.; Mosaic structure of globular domains in the human type VI collagen alpha 3 chain: similarity to von Willebrand factor, fibronectin, actin, salivary proteins and aprotinin type protease inhibitors."; EMBO J. 9:385-393(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             timpl R.; ^{\prime} *Amino acid sequence of the triple-helical domain of human collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chu M.-L., Conway D., Pan T.-C., Baldwin C., Mann K., Deutzmann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88161046; PubMed=3348212; Weil D., Mattei M.-G., Passage B., van Cong N., Pribula-Conway D., Mann K., Deutzmann R., Timpl R., Chu M.-L.; Chu diromosomal localization of human genes encoding the three chains of type VI collagen.";
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chu M.-L.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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                                                           CA36_HUMAN STANDARD; PRT; 3176 AA. P12111; Q16501; 01-0CT-1989 (Rel. 12, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Collagen alpha 3(VI) chain precursor.
                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 267:24082-24089(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 263:18601-18606(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 168:309-317(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Am. J. Hum. Genet. 42:435-445 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2038-2373 FROM N.A. MEDLINE=89066644; PubMed=3198591;
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                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fibroblast;
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               RESULT 11
CA36 HUMAN
1D CA36 HUMAN
1D CA36 HUMAN
1D C1 10-0CT-1
DT 15-0CT-1
DT 15-0CT-1
DT 10-0CT-1
DT
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Rolar Tab.

The Tructure and multiple conformations of the Kunitz-type domain from human type VV collegen alpha3 (VI) chain in solution.;

The Multiple VV collegen alpha3 (VI) chain in solution.;

Man Serensen W. V. Diolen P. S. Naris A. Olen O., Petersen L.,

Socrensen W. W. Diolen P. S. Naris A. Olen O., Petersen L.,

Socrensen W. D. Bjoern P. S. Naris A. Olen O., Petersen L.,

Socrensen W. D. Bjoern P. S. Naris A. Olen O., Petersen L.,

MEDITE-2189763 (1937).

Man Julian Genet. Joint Abackbook dynamics of the human alpha3-chain processing the man alpha3-chain and the man alpha3-chain alph
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ACCOUNTED TO THE STATE OF THE STATE OF THE STATE OF STATE
                      LHKTLQPLVKRVCDTDRLACSKTCLNSADIGPVIDGSSSVGTGNFRTVLQFVTNLTKRFE 526
                                            527 ISDTDTRIGAVQYTYBORLBFGFDKYSSKPDILNAIKRVGYWSGG--TSTGAAINFALEQ 584
                                                                                                                                  585 LFKKSKPNK-----RKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVI 639
                                                                                                                                                                                                                    | :: :: :: :: :: | | | | :| :| 333 HFTRAGGSRVERGUPULISAGPSSBIRYGWVALKQASVFSFGLGAQAASRABLQHI 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUE=Embryonic kidney;
MEDILINE=99043741; PubMed=9827539;
Wagner R., Kobbe B., Paulsson M.;
Wenomic organisation, alternative splicing and primary structure of human matrilin-4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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-!- FUNCTION: Major component of the extracellular matrix of
                                                                                                                                                                                                                                                                                 640 ATHPARDHSFFVDEFDNIHQYVPRIIQNICTEFNS 674
                                                                                                                                                                                                                                                                                                                         393 ATD-----BERS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                MTN4 HUMAN STANDARD; PRT; 619 AA. 095460; 0991RB; Q9H1F9; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEBS Lett. 438:165-170(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matrilin-4 precursor. MATN4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: ||:| | : ||: ||: ||: ||: || || :| || 39 DIIPLYDSSWIIGEEHPQLYREFLYDVVKSLAVGENDPHPALVQFNGNPHTEFLLNTYRT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 DLSFLIDGSTSIGKRRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 SRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGNRS--GAPNVVVWWVDGWPTDKV
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SIGNAL
SIGNAL
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NONHELICAL REGION.
TRIPLE-HELICAL REGION.
NONHELICAL REGION.
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FIBRONECTIN TYPE-III.
BPTI/KUNITZ INHIBITOR.
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REACTIVE BOND.
                                                                              MINA; 20100589; C:collagen type VI; TAS.
GO; GO:0007517; P:muscle development; TAS.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clg helix.
InterPro; IPR003261; FN III.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002233; Kunitz_BPTI.
InterPro; IPR002235; WWF A.
Pfam; PP010191; Collagen; S.
Pfam; PP010191; Collagen; S.
Pfam; PP00024; WWF III.
PRINTS; PR00759; BASICPTASE.
PRINTS; PR00759; WFPADOMAIN.
ProDom; PD000007; Clg helix; 2.
ProDom; PD000007; Clg helix; 2.
ProDom; PD000022; Kunitz_BPTI; 1.
SMART; SM00131; KU; 1.
SMART; SM00131; KU; 1.
PROSITE; PS50280; BPTI KUNITZ_1; 1.
PROSITE; PS50280; BPTI KUNITZ_2; 1.
PROSITE; PS50234; VWFA; 12.
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VWFA 2.
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Genew; HGNC:2213; COL6A3
MIM; 120250; -.
MIM; 158810; -.
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LEP----VSLGDPNC---KIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPAGFLM 332
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                                                                                                                                                                                                                                                                                                                                     254 SIDICAEGTRGCEHHCVNSPGSYPCHCQVGFVLQQDQRSCRAIDYCSPGNHSCQHBCVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545 LEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINPALEQLFKK---SKP---NKRKLMI
                               SECUENCE FROM N.A. (ISOFORM LONG).
STRAIN=C57BL/6J; TISSUB-Mammary gland;
MEDLINE=22388257; Pubmed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                         --DRLA----CSKTCLNS-----ADIGFV------
                                                                                                   GVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGNR-
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STRAIN=C57BL/6J, and CD-1; TISSTR=Fetal;
MEDLINE=98442849; PubMed=9711906;
WAGENER R., Kobbe B., Paulsson M.;
"Matrilin-4, a new member of the matrilin family of extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIN4_MOUSE STANDARD; PRT; 624 AA. 089029; 0890319; 090783; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Matrilin-4 precursor (WAT-4).
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FEBS Lett. 436:123-127(1998)
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MTN4 MOUSE
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                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R GO, GO: GO: GOOSSTO, C: extracellular; TAS.

R GO; GO: GO: GOOSSTO, C: extracellular; TAS.

R InterPro; IPR001821; EGF_Ca.

R InterPro; IPR001821; EGF_Ca.

R InterPro; IPR002035; VWF_A.

R Pfam; PF00092; Vwa; 2.

R Pfam; PR00923; VWFADOMAIN.

R Pfam; PR00921; VWADOMAIN.

R SWART; SW00179; EGF_CA; 1.

R SWART; SW00179; EGF_CA; 1.

R SWART; SW00191; EGF_CA; 1.

R PROSITE; PS00186; EGF_2; 1.

R PROSITE; PS00186; EGF_2; 1.

R PROSITE; PS0186; EGF_2; 1.

R PROSITE; PS0186; EGF_2; 1.

R PROSITE; PS0234; VWFA; 2.

R PROSITE; PS0234; VWFA; 2.

R PROSITE; PS0186; EGF_2; 1.

R RGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil; I.

R SIGNAL
                                                                                                                        IsoId=095460-2; Sequence=VSP 001400;
-!- TISSUE SPECIFICITY: Bhiryonic Kidney, lung and placenta.
-!- SIMILARITY: Contains 4 EGF-like domains.
-!- SIMILARITY: Contains 2 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> S (IN REF. 1).
-> NL (IN REF. 1).
2FICE3C9CCC54B5D CRC64;
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  Bvent=Alternative splicing, Named isoforms=2;
Comment=Additional isoforms seem to exist;
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MATRILIN-4.
VWFA 1.
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EGF-LIKE 3.
EGF-LIKE 4.
                                                                            IsoId=095460-1; Sequence=Displayed;
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Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Lung, brain, sternum, kidney and heart. DEVELOPMENTAL STAGE: The short isoform was detected in 7 weeks old mice but not in developing mice (19.5 dpc embryos or in 2, 8, and 21 days old animals).
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
               Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Halls S., Garcia A.M., Gap L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butteffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., "Generchion and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                 MEDLINE=99043241; PubMed=9827539;
Wagener R., Kobbe B., Paulsson M.;
"Genomic organisation, alternative splicing and primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMEL; AJ006140; CAA06899.1; --
R EMEL; AJ006140; CAA06899.1; --
R EMEL; AJ006140; CAA06899.1; --
R EMEL; AJ006140; CAA0689.1; --
R EMEL; AJ010984; CAA09451.1; --
R HSSP; P00736; 1APO.
R INCEPTO; IPRO00152; ARA hydroxyl_S.
R INCEPTO; IPRO002035; VWF_A.
R INCEPTO; IPRO002035; VWF_A.
R INCEPTO; IPRO002035; VWF_A.
R Pfam; PP000092; VWF_A.
R Pfam; PP000092; VWF_A.
R PAMNTS; PR00413; VWFADOWAIN.
R SWART; SW00327; VWF_A.
R PROSITE; PS01186; BGF_2; 2.
R PROSITE; PS01186; BGF_2; 2.
R PROSITE; PS01186; BGF_2; 2.
R RGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil;
T CHAIN 22 624 MATRILIN-4.
T CHAIN 36 215 VWFA 1.
T DOMAIN 36 215 VWFA 1.
T DOMAIN 37 225
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                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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EGP-LIKE 2.
EGP-LIKE 3.
EGP-LIKE 4.
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484 LACSKTCLNSADIGFVIDGSSSYGTGNFRTVLQFVTNLTKEFRISDTRIGAVQYTVBQ 543
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BY SIMILARITY.
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71; Mismatches 199; Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                            11.8%; Score 412.5; DB 1; Length 624;
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Last annotation update)
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Matches 125; Conservative
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                                                                           PubMed=11124542;
A Muratcglu S., Krysan K., Balazs M., Sheng H., Zakany R., Modis L.,
A Kiss I., Deak P.,
X Kiss I., Deak P.,
X Kiss I., Deak P.,
Yiss I., Deak P.,
Yiss I., Deak P.,
Yiss I., Deak P.,
Yorgenet. Cell Genet. 90:323-327(2000).

Cytogenet. Cell Genet. 90:323-327(2000).

REDLINE-9723863; PubMed=9083061;
P. SEQUENCE OF 644-9988061;
A Deak P., Piacha D., Bachrati C., Paulsson M., Kiss I.;
Primary structure and expression of matrilin-2, the closest relative of cartilage matrix protein within the von Willebrand factor type A-
I like module superfamily.";
J. Biol. Chem. 272:9268-9274(1997).
                                                                                                                                                                                                                                                                          Duesterhoeff A., Lauber J., Meves H.-W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: Involved in matrix assembly (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
        Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00010; ASX_HYDROXYL; 9.

PROSITE; PS01186; BCF_2; 9.

PROSITE; PS50234; VWFA; 2.

PROSITE; PS50234; VWFA; 3.

PROSITE : PS50234; VWFA; 3.

PSTENTIAL.
                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                    Name=Short;
Isoid=C00339-2; Sequence=VSP 001399;
--- SIMILARITY: Contains 10 EGF-11Ke domains.
--- SIMILARITY: Contains 2 VWPA domains.
                                                        [1] SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 602108; -.
GO; GO:0005578; C:extracellular matrix; NAS.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR001881; BGP Ca.
InterPro; IPR005209; BGP Tike.
InterPro; IPR005209; BGP Tike.
Pfam; PF00008; BGP; 10.
Pfam; PF000092; vwa; 2.
                                                                                                                                                                                                                                                                                                                                               Name=Long;
Isoid=000339-1; Sequence=Displayed;
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VWPA 1.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
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HSSP; P01132; 1EGF.
Genew; HGNC:6908; MATN2.
                                                                                                                                                                                                                                                     SEQUENCE OF 244-956 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZMBL; U69263; AAC51260.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0453; WWFADGMAIN.
SMART; SM00179; EGF_CA; 1.
SMART; SM00327; VWA; 2.
                                         NCBI_TaxID=9606;
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256 APQKPVGADVSLGLVPKERLSTQSLRPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQL 315
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260 YVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDGRRCV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 DENTLKSIGSEPHEDHVFLVANFSQIRTLTSVFQKKLCTAHMCSTLEHNCAHFCINIPGS 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 LADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIBKITQRGGLSNVGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 ISFVTKNFFSKANGN---RSGAPNVVVVNVVVNVDGWPTDKVBEASRLARESGINIF----
                                                                                                                                         WE SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform Short).
/PTIGLAVEP 001399.
K -> B (IN RBF. 3).
V -> B (IN RBF. 3).
R -> G (IN RBF. 3).
F -> L (IN RBF. 3).
L -> F (IN RBF. 3).
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BGF-LIKE 5.
BGF-LIKE 6.
BGF-LIKE 7.
EGF-LIKE 9.
BGF-LIKE 10.
VWPA 2.
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956 AA;
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Pred. No. 2.4e-14;
; Mismatches 177; Indels 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00010; ASX_HYDROXXL; 7.
PROSITE; PS01186; BGP_2; 9.
PROSITE; PS50234; WWFA; 2.
BGP-1ke domain; Signal; Glycoprotein; Repeat; Coiled coil.
23
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BGP-LIKE 2.
BGP-LIKE 3.
BGP-LIKE 4.
BGP-LIKE 6.
BGP-LIKE 6.
BGP-LIKE 7.
BGP-LIKE 9.
BGP-LIKE 9.
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send an email to license@isb-sib.ch)
                                                                                                                 MGD; MGI:109613; Matn2.
GO; GO:0005578; C:extracellular ma
InterPro; IPR0010152; Asx hydroxyl,
InterPro; IPR00181; BGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
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                                                                                                                                                                                                                                                                                              InterPro; IPR002035; VWP_A. Pfam; PP00008; BGF; 10. Pfam; PP00022; Vwa; 2. PRINTS; PR00453; VWFDCWAIN. SWART; SM00181; BGF; 10. SWART; SM00327; VWA; 2.
                                                     EMBL; U69262; AAC53163.1; -. HSSP; P05099; 1AQ5.
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Matches 140; Conservative
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X MEDLINE=97238863; PubMed=9083061;
A Deak F., Piecha D., Bachrati C., Paulsson M., Kiss I.;
Deak F., Piecha D., Bachrati C., Paulsson M., Kiss I.;
Deak F., Piecha D., Bachrati C., Paulsson M., Kiss I.;

of cartilage matrix protein within the von Willebrand factor type A-
Iike module superfamily.

I ike module superfamily.

i J. Biol. Chem. 272:9268-9274(1997).

c. I FUNCTION: Involved in matrix assembly (By similarity).

c. I FUNCTION: Detected in a variety of organs, including calvaria, uterus, heart and brain, as well as fibroblast and calvaria. terus.

c. I TISSUB SPECIFICITY: Detected in a variety of organs, including calvaria uterus, heart and brain, as well as fibroblast and conteoblast cell lines.

c. I SIMILARITY: Contains 10 EGP-like domains.
                                                              320 AVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDKKTCTKIDYCASSNHGCQHECVNT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 DGKICRRKDVCQAIDHGCEHICVNSDDSYTCECLVGPRLAEDGKRCRRKDVCKSTHHGCE 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       620 HICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGBENFRVVKQFVT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAIN 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680 GIIDSLTISPKAARVGILQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMTGLALK 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDSYSCHCLKGFTLNPDKKTCRRINYCALNKPGCEHECVNWEBSYYCRCHRGYTLDPWGK 439
                                                                                                                                                                                                                                                                                                       440 TCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSC 499
                                                                                                                                                                                                                                                                                                                                                                                                                           500 VNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSCVSSEDSFVCQCFEGYILRE 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KRVCDTDRLACS 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALEQLEKK---SKPNKRKL---MILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQ 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 KTCLNSA------DIGFVIDGSSSVGTGNFRTVLQFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNIC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | : | | : | | | : : | | BELQEIASEPTINGHLFYARDFSTWDBISEKLKKGIC 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         454 NGFYSLHVQSWPGL-----
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                                                                                                                                                                                                                                                     Matrilin-2 precursor.
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14;

Gaps

169 LVPKEBLSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDIGPA 328 	129 GPLAGUVQYGDNPATHFNLKTHTNSRDLKTALEKTTQRGGLSNVGRAISFVTKNFFSKAN 388 	389 GNRSGAPNVVVVWVDGWPTDKVEBASRLARESGINIP	.26PITIEG	32	36BKQYVVB	53		60 -HVQSWPGIAKTLQPL	75 494 71 QDVNHGCEHLCVNSGESYVCKCLEGFRLAEDGKRCRRKNVCKSTQHGCEHMCVNNGNSYL 630	95	31 DTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFKKSK 590 	91PNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQBELEVIATHPA 644 : :: :	45 RDHSFFVDEFDNLHQYVPRIIQNIC 669 : : :
269 LV	329 GI 93 VI	389 GP 	426	432 273 DC	436 333 HE	453	453	460 -F	475 571 QE	495	531 DT 691 AZ	591 751 G	645 RE 811 DF
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Search completed: May 27, 2004, 16:44:47 Job time : 26 secs

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certaine (c) 1000 - 2001 Compagent aca.	19 8 1.2 285 16	6 Q92MJ9	Q92mj9 rhizobium m
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rotein search, using sw model	22 8 1.2 382 12	2 083907	O83907 Ovine adeno
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Caithout Came of Medical	24 8 1.2 394 16	6 Q97FB4	Q97fe4 clostridium
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1 MRIVVLIMKASVIEMFIJJ.		Q9HEC6	O9hec6 neurospora
	30 8 1.2 462 2	Q8RMG7	Q8rmg7 acetobacter
OFIGO	31 8 1.2 494 4	096IU6	Q961u6 homo sapien
Gapop 60.0 , Gapext 60.0		o	Q9h647 homo sapien
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	35 8 1.2 686 5	Q9W013	Q9w013 drosophila
	36 8 1.2 695 16	5 09СН87	Q9ch87 lactococcus
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f hits satisfying chosen parameters:	200	C360Y7	Q960y7 drosophila
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	42 8 1.2 1464 5	096782	096782 drosophila
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SPTREMBL 25:*	45 7 1.0 34 4	оэнзкв	Q9h3r8 homo sapien

Total number of hits satisfying chosen parameters:

Word size : Ware 6

Searched:

Post-processing: Listing first 45 summaries

Database:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Title: Perfect score:

Sequence:

Scoring table:

- protein search, using sw model

OM protein

Run on:

ALIGNMENTS

678 AA

Similar to Coch-582. WUGSC:H WHO294L11.1. Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. WaterEron R.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO7363; AAF19243.1; -.
EMSP; Pl1115; JUZM.
InterPro; IPR004043; LCCL dom.
InterPro; IPR002035; VWFĀ.
Pfam; PP00315; LCCL; 1.
Pfam; PP00921; VWFADOMAIN.
SWART; SM00603; LCCL; 1.
SWART; SM00327; VWA; 2.
PROSITE; PS50234; VWPA, 2.
PROSITE; PS50234; VWPA, 2. SEQUENCE FROM N.A.
Cordes M., Kalicki J., Ames M.;
"The sequence of Homo sapiens BAC clone RP11-294L11.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases Lisates, Last sequence update) Last annotation update) SEQUENCE FROM N.A.
MEDLINE-99063792; Pubwed=9847074;
Sulston J.E., Waterston R.;
"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108(1998). Created) PRT; Q9UDNO; 01-MAY-2000 (TrEMBLrel: 13, 01-MAY-2000 (TrEMBLrel: 13, 01-MAR-2003 (TrEMBLrel: 23, PRELIMINARY; SEQUENCE FROM N.A. NCBI_TaxID=9606; Q9UDN0 RESULT 1 Q9UDNO 087his mus musculu 08aws6 brachydanio 08hy2 oryza sativ 08578 bifidobacte 09cb89 mycobacteri 090zy9 brachydanio 054667 streptococc 08kwq1 streptococc Q9udnO homo sapien Q96dmB homo sapien Q96dtl homo sapien Q95112 bos taurus Q8bq41 mus musculu Q8kd47 mus musculu Q9cyz1 mus musculu Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES Q9UDNO Q96DMB Q96DT1 Q95L12 Q8EQ41 Q9CYZ1 Q8CYZ1 Q8CYZ1 Q8CYZ1 Q8CYZ1 Q8CYZ1 Q8CYZ1 Q8CYZ1 Q8CYZ1 Q8CZYB Q9CZYB Q9CZYB Q9CZYB sp_archea:*
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181 181 241 241 301 301 361 361

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328 AGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIBKITQRGGLSNVGRAISFVTKNFFSKA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 GLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRFFIQKQLLADVAQALDIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGNRSGAPNVVVVMVDGWPTDKVERASRLARESGINIFFITIEGAARNEKQYVVBPNFAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 TGNFRIVLQEVINLIKEPEISDIDIRIGAVQYIYEQRLEFGFDKYSSKPDILNAIKRVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 WSGGISICAAINFALEQLFKKSKPNKRKIMILIIDGRSYDDVRIPAMAAHLKGVIIYAIG
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                       Yamamoto J., Isono Y., Kawal-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujil A., Oshima A., Sugiyama A., Kawakami E
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
EMBL; AKO56772; BAB11279.1; -.
EMBL; AKO56772; BAB11279.1; -.
InterPro; IPR0004043; LCCL dom.
InterPro; IPR0004043; LCCL dom.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
   Sato H., Wakamatsu A., Ishii S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     628 VAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN 678
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TISSUE-Skeletal muscle, and Fetal heart;
Ren Z.-X., Liu J.G., Mayne R.;
"Human vitrin complete cDNA sequence.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75575 MW; 2DE8B2421F2D496D CRC64;
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Last annotation update)
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Sugiyama T., Irie R., Otsuki T.,
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(TrEMBLrel. 19,
(TrEMBLrel. 23,
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SMART; SM00603; LCCL; 1.
SMART; SM00327; VWA; 2.
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PROSITE; PS50234; VWFA; 2.
Hypothetical protein.
SEQUENCE 693 AA; 75575
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Pfam; PF00092; vwa; 2.
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01-DEC-2001 (
01-MAR-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VQSLSLPRWRESPIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKITORGGLSNVGRAISFVTKNFFSKANGNRSGAPNVVVVWWDGWPTDKVBEASRLARES 420
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                                                                                                                                                                                                                                  1 MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIV
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                  ö
                                                             100.0%; Score 678; DB 4; Length 678; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0
   73930 MW; 9870E75A218C686C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ32210.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPRIIQNICTEFNSQPRN 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPRIIONICTEFNSOPRN
                                                                                                                              Matches 678; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
678 AA;
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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421

421

481 541 541 601

481

661 661

RESULT 2

Q96DM8

601

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327 342 402 447 462 507 522 567 582 627 642

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TISSUE-Placenta; Linhbashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Ebitita T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Rotanabe M., Pujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,